

Result No.	Score	Query Match Length	DB ID	Description
1	753	99.1	156	cyclin dependent kinase inhibitor - human
2	529	69.6	2	CDK4 inhibitor p14
3	522	68.7	138	p15INK4a - mouse
4	461.5	60.7	167	cyclin-dependent kinase inhibitor
5	258	33.9	164	cyclin-dependent kinase inhibitor
6	249	32.8	166	cyclin-dependent kinase inhibitor
7	244	32.1	166	cyclin-dependent kinase inhibitor
8	231.5	30.5	168	CDK6 inhibitor p18
9	228.5	30.1	168	gene p15INK4b prot
10	209	27.5	152720	ankyrin 2, neuron
11	158	20.8	3924	ankyrin 1, erythrocyte
12	137.5	18.1	1848	potassium channel
13	137.5	18.1	1862	death-associated protein
14	133.5	17.6	1856	potassium channel
15	133.5	17.6	1880	ankyrin 1, erythrocyte
16	133.5	17.6	1881	potassium channel
17	131	17.2	857	ankyrin 3, long sp
18	130.5	17.2	1423	elegans ankyrin-related protein
19	130	17.1	838	ankyrin 3, splice
20	130	17.1	1765	ankyrin 3, splice
21	130	17.1	1940	ankyrin 3, splice
22	130	17.1	1943	ankyrin 3, splice
23	130	17.1	1961	ankyrin 3, splice
24	128	16.8	4377	ankyrin 3, long sp
25	127.5	16.8	1786	elegans ankyrin-related protein
26	127.5	16.8	1815	ankyrin repeat proteins; ankyrin repeat domain
27	127.5	16.8	1867	ankyrin repeat domain
28	127.5	16.8	2039	ankyrin repeat domain
29	126	16.6	247	ankyrin-related protein

ALIGNMENTS						
RESULT	1					
JE0141						
cyclin dependent kinase inhibitor - human						
N;Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor						
C;Species: Homo sapiens (man)						
C;Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000						
C;Accession: JE0141; I5268; S39359; I59585; JC5679						
R;Huang, C.G.; Deng, W.; Fu, J.L.						
Chin, J. Biotechnol. 13, 105-107, 1997						
A;Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.						
A;Reference number: JE0141						
A;Accession: JE0141						
A;Molecule type: mRNA						
A;Residues: 1-156 <HUA>						
A;Experimental source: Hella cell						
R;Okamoto, A.; Demerick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, R;Serrano, M.; Hannon, G.J.; Beach, D.						
proc. Natl. Acad. Sci. U.S.A. 91, 11005-11049, 1994						
A;Title: Mutations and altered expression of p16INK4 in human cancer.						
A;Reference number: I59268; MUID:95062202						
A;Accession: I59268						
A;Status: translation not shown; translated from GB/EMBL/DBJ						
A;Molecule type: DNA						
A;Residues: 1-152 <OKA>						
A;Cross-references: GB:L27211; NID:9558656; PID:9558657						
A;Note: the sequence is revised in Genbank entry HUMINK4X, release 113.0, PID:AAA925						
R;Serrano, M.; Hannon, G.J.; Beach, D.						
Nature 366, 704-707, 1993						
A;Title: A new regulatory motif in cell-cycle control causing specific inhibition of						
A;Reference number: S39359; MUID:94081956						
A;Accession: S39359						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 9-34, 'V', 36-156 <SER>						
A;Note: this sequence is corrected in reference I59268						
R;Kamb, A.; Grull, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;						
Science 264, 436-440, 1994						
A;Title: A Cell cycle regulator potentially involved in genesis of many tumor types.						
A;Reference number: I59585						
A;Accession: I59585						
A;Status: translation not shown; translated from GB/EMBL/DBJ						
A;Molecule type: DNA						
A;Residues: 51-152 <KAM>						
A;Cross-references: GB:S69804; PID:9546272; PID:AAD1404B.1; PID:94261748						
C;Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 ki						
C;Genetics:						
A;Gene: GDB:CDKN2A; CDK4I; MLL; P16; INK4; MTS1; OMIM:500160						
A;Cross-references: GDB:335362; OMIM:500160						
A;Map position: 9p21-9p21						
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homolog						
C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor						

Query Match 99.1%; Score 753; DB 2; Length 156;
 Best Local Similarity 99.3%; Pred. No. 1.5e-64; Indels 0; Gaps 0;
 Matches 147; Conservative 0; Mismatches 1; DB 9
 A; Cross-references: GB:L36844; NID:9556197; PIDN:AAA50287.1; PID:9556198
 A; Experimental source: Hacat cells
 R; Kamb, A.; Grus, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;
 Science 264, 436-440, 1994
 A; Title: A cell cycle regulator potentially involved in genesis of many tumor types.
 A; Reference number: I59585; MUID:94204645
 A; Accession: 181183
 A; Status: translation not shown; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 53-138 <KAN>
 A; Cross-references: GB:S659805; NID:9546273; PIDN:AAD14049.1; PID:94261749
 R; Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.;
 Cancer Res. 54, 633-6358, 1994
 A; Title: Deletion of p16 and p15 genes in brain tumors.
 A; Reference number: I52213; MUID:9507408
 A; Accession: I52713
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-52 <RES>
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 C; Genetics:
 A; Gene: GDB:CDKN2B; MTSS2
 A; Cross-references: GDB:579577; OMIM:600431
 A; Map position: 9p21-9p21
 C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
 C; Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

RESULT 2

I7845
 p15INK4b - mouse
 C;Species: Mus sp. (mouse)
 C;Date: 02-Aug-1996 #sequence_change 02-Aug-1996 #text_change 19-May-2000
 C;Accession: I78845
 R;Quelle, D.E.; Ashmun, R.A.; Hannan, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W
 Oncogene 11, 635-645, 1995
 A;Title: Cloning and characterization of murine p15INK4a and p15INK4b genes.
 A;Reference number: I58352; MUID:9530169
 A;Accession: I78845
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-130 <RES>
 A;Cross-references: GB:S79252; NID:91087092; PID:91087093
 C;Genet.cs:
 A;Gene: p15INK4b
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 Query Match 69.6%; Score 529; DB 2; Length 130;
 Best Local Similarity 68.3%; Pred. No. 2.3e-43; Indels 0; Gaps 0;
 Matches 106; Conservative 4; Mismatches 10; DB 10
 A; Cross-references: GB:S79252; NID:91087092; PID:91087093
 C;Species: Mus sp. (mouse)
 C;Accession: I58352
 R;Quelle, D.E.; Ashmun, R.A.; Hannan, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.
 Oncogene 11, 635-645, 1995
 A;Title: Cloning and characterization of murine p16INK4a and p16INK4b genes.
 A;Reference number: I58352; MUID:9530169
 A;Accession: I58352
 A;Molecule type: mRNA
 A;Residues: 1-167 <RES>
 A;Cross-references: GB:S79251; NID:91087090; PID:91087091
 C;Genetics:
 A;Gene: p16INK4a
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

RESULT 3

B55479
 CDK4 inhibitor p14(INK4B/MTS2) - human
 N;Alternate names: CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor
 C;Species: Homo sapiens (man)
 C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000
 C;Accession: B55479; S47593; I81183; I52713
 R;Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;
 Genes Dev. 8, 2939-2952, 1994
 A;Title: Growth suppression by p18, a p16(INK4B/MTS2)-related CDK6 i
 A;Reference number: A55479; MUID:95095079
 A;Accession: B55479
 A;Molecule type: mRNA
 A;Residues: 1-138 <5UA>
 A;Cross-references: GB:U17075; NID:9639715; PIDN:AAC50075.1; PID:9639716
 A;Experimental source: HeLa cells
 R;Hannan, G.J.; Beach, D.
 Nature 371, 257-261, 1994
 A;Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.
 A;Reference number: S47593; MUID:94359613
 A;Accession: S47593
 A;Molecule type: mRNA
 A;Residues: 1-19, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>

Query Match 60.7%; Score 461.5; DB 2; Length 167;
 Best Local Similarity 63.2%; Pred. No. 8.5e-37; Mismatches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;
 C;Species: Mus sp. (mouse)
 C;Accession: I58352
 R;Quelle, D.E.; Ashmun, R.A.; Hannan, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.
 Oncogene 11, 635-645, 1995
 A;Title: Cloning and characterization of murine p16INK4a and p16INK4b genes.
 A;Reference number: I58352; MUID:9530169
 A;Accession: I58352
 A;Molecule type: mRNA
 A;Residues: 1-167 <RES>
 A;Cross-references: GB:S79251; NID:91087090; PID:91087091
 C;Genetics:
 A;Gene: p16INK4a
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

RESULT 4

I58352
 p16INK4a - mouse
 C;Species: Mus sp. (mouse)
 C;Accession: I58352
 R;Quelle, D.E.; Ashmun, R.A.; Hannan, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.
 Oncogene 11, 635-645, 1995
 A;Title: Cloning and characterization of murine p16INK4a and p16INK4b genes.
 A;Reference number: I58352; MUID:9530169
 A;Accession: I58352
 A;Molecule type: mRNA
 A;Residues: 1-167 <RES>
 A;Cross-references: GB:S79251; NID:91087090; PID:91087091
 C;Genetics:
 A;Gene: p16INK4a
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

Query Match 60.7%; Score 461.5; DB 2; Length 167;
 Best Local Similarity 63.2%; Pred. No. 8.5e-37; Mismatches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;
 C;Species: Mus sp. (mouse)
 C;Accession: I58352
 R;Quelle, D.E.; Ashmun, R.A.; Hannan, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.
 Oncogene 11, 635-645, 1995
 A;Title: Cloning and characterization of murine p16INK4a and p16INK4b genes.
 A;Reference number: I58352; MUID:9530169
 A;Accession: I58352
 A;Molecule type: mRNA
 A;Residues: 1-167 <RES>
 A;Cross-references: GB:S79251; NID:91087090; PID:91087091
 C;Genetics:
 A;Gene: p16INK4a
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

RESULT 5

QY 1 MEPSADWIAATAAARGRVEEVRAVALLPAVLNAPNSYGRPPIQVMMGSARVAELLILLHGAPRN 60
 Db 1 MEQAADRLLA-RAAQGRVHDRAVALLAEAGVSPNAPNSFGRTP1QVMAMNGNVHYAALLLNNGA 59

Qy	61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL-	Qy	65 ADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL-
Db	: : : : : : : : : : : : : :	Db	: : : : : : : : : : : : : :
Qy	60 DSNCEDPTFSRPHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL-	Db	70 QD-ASGTSVHDAARTGLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL-
C;Species:	Homo sapiens (man)	C;Species:	Mus musculus (house mouse)
C;Date:	08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999	C;Date:	08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
C;Accession:	A57378	C;Accession:	B57378
R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.	R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.	Mol. Cell. Biol. 15, 2682-2688, 1995	Mol. Cell. Biol. 15, 2682-2688, 1995
A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19
A;Reference number: A57378; MUID:95257949			
A;Accession:	A57378	A;Accession:	B57378
A;Status: preliminary	A;Status: preliminary	A;Status: preliminary	A;Status: preliminary
A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA
A;Residues: 1-166 <CHA>	A;Residues: 1-166 <CHA>	A;Residues: 1-166 <CHA>	A;Residues: 1-166 <CHA>
A;Cross-references: GB:U204986	A;Cross-references: GB:U204986	A;Cross-references: GB:U204976	A;Cross-references: GB:U204976
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A;Map position: 19q13	A;Map position: 19q13	A;Map position: 19q13	A;Map position: 19q13
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
RESULT 5		RESULT 7	
A57378		B57378	
cyclin-dependent kinase inhibitor p19 - human	cyclin-dependent kinase inhibitor p19 - mouse	cyclin-dependent kinase inhibitor p19 - mouse	cyclin-dependent kinase inhibitor p19 - mouse
C;Species: Homo sapiens (man)	C;Species: Mus musculus (house mouse)	C;Species: Mus musculus (house mouse)	C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999			
C;Accession: A57378	C;Accession: B57378	C;Accession: B57378	C;Accession: B57378
R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.	R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.	Mol. Cell. Biol. 15, 2682-2688, 1995	Mol. Cell. Biol. 15, 2682-2688, 1995
A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19	A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to cyclin-dependent kinase inhibitor p19
A;Reference number: A57378; MUID:95257949			
A;Accession:	A;Accession:	A;Accession:	A;Accession:
A;Status: preliminary	A;Status: preliminary	A;Status: preliminary	A;Status: preliminary
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A;Map position: 19q13	A;Map position: 19q13	A;Map position: 19q13	A;Map position: 19q13
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
Query Match 33.9%; Score 258; DB 2; Length 164;	Query Match 32.1%; Score 244; DB 2; Length 166;	Query Match 32.1%; Score 244; DB 2; Length 166;	Query Match 32.1%; Score 244; DB 2; Length 166;
Best Local Similarity 44.1%; Pred. No. 1.8e-17; Mismatches 67; Indels 6; Gaps 3;	Best Local Similarity 43.7%; Pred. No. 4e-16; Mismatches 69; Indels 18; Gaps 5;	Best Local Similarity 43.7%; Pred. No. 4e-16; Mismatches 53; Indels 18; Gaps 5;	Best Local Similarity 43.7%; Pred. No. 4e-16; Mismatches 53; Indels 18; Gaps 5;
Matches 67; Conservative 17; Mismatches 62; Indels 6; Gaps 3;	Matches 69; Conservative 18; Mismatches 53; Indels 18; Gaps 5;	Matches 69; Conservative 18; Mismatches 53; Indels 18; Gaps 5;	Matches 69; Conservative 18; Mismatches 53; Indels 18; Gaps 5;
Qy 2 EPSADWLAARRGVVEYRALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 60	Qy 6 DWLATAAAARGRVEEVRAALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 64	Qy 6 DWLATAAAARGRVEEVRAALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 64	Qy 6 DWLATAAAARGRVEEVRAALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 64
Db 5 EVRAGTLSQAARDSDVQVRLLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 64	Db 10 DRLSGARPGDVOVRLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 64	Db 10 DRLSGARPGDVOVRLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 64	Db 10 DRLSGARPGDVOVRLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 64
Qy 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL	Qy 65 ADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL	Qy 65 ADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL	Qy 65 ADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRAWRGLPVDLAELGLHRDVARYL
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Qy 121 YLRAAAAG---GTRGSNHARIDAAGEPSIDP 148	Db 129 ESDLHHRDASGLTPLEALARQGAQNL-MDILOQGHMMTP 165	Db 129 ESDLHHRDASGLTPLEALARQGAQNL-MDILOQGHMMTP 165	Db 129 ESDLHHRDASGLTPLEALARQGAQNL-MDILOQGHMMTP 165
Db 124 FLAAESDLHRRDARGLTPLEALARQGAQDLV 155			
RESULT 8		RESULT 8	
B57379		B57379	
CDK4/CDK6 inhibitor p18 - mouse			
C;Species: Mus musculus (house mouse)			
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999			
C;Accession: A57379	C;Accession: B57379	C;Accession: B57379	C;Accession: B57379
R;Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.	R;Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.	R;Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.	R;Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Mol. Cell. Biol. 15, 2672-2681, 1995			
A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de	A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de	A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de	A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de
A;Reference number: A57379; MUID:95257948			
A;Accession:	A;Accession:	A;Accession:	A;Accession:
A;Status: preliminary	A;Status: preliminary	A;Status: preliminary	A;Status: preliminary
A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA	A;Molecule type: mRNA
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C;Keywords: cell cycle control			
Query Match 30.5%; Score 231.5; DB 2; Length 168;	Query Match 30.5%; Score 231.5; DB 2; Length 168;	Query Match 30.5%; Score 231.5; DB 2; Length 168;	Query Match 30.5%; Score 231.5; DB 2; Length 168;
Best Local Similarity 40.3%; Pred. No. 6.2e-15; Mismatches 56; Indels 1; Gaps 1;	Best Local Similarity 40.3%; Pred. No. 6.2e-15; Mismatches 56; Indels 1; Gaps 1;	Best Local Similarity 40.3%; Pred. No. 6.2e-15; Mismatches 56; Indels 1; Gaps 1;	Best Local Similarity 40.3%; Pred. No. 6.2e-15; Mismatches 56; Indels 1; Gaps 1;
Matches 56; Conservative 22; MisMatches 60; Indels 1; Gaps 1;	Matches 56; Conservative 22; MisMatches 60; Indels 1; Gaps 1;	Matches 56; Conservative 22; MisMatches 60; Indels 1; Gaps 1;	Matches 56; Conservative 22; MisMatches 60; Indels 1; Gaps 1;
Qy 2 EPSADWLAARRGVVEYRALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 61			
Db 3 EPWNGEFLASAARRDQEVRLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 62			
Qy 6 DWLATAAAARGRVEEVRAALL-EAVALPNAPNSYGRPPQMMMGSAVARAEELLLHGAEPNC 64			
Db 10 DRLSGARPGDVOVRLHRELVHPDALNRECKTALQVMMFGSTAFALELIKOGA 65			

F;562-594/Domain: ankyrin repeat homology <AN16>	Qy 8 LATAAARGRVEEVRALEAVALPNAPNSYGRPPIQV-MMMGSARVAELLLLHGAEPNCA 66
F;595-627/Domain: ankyrin repeat homology <AN17>	: : : : : : : : : : : : : : : : : : :
F;628-660/Domain: ankyrin repeat homology <AN18>	Db 511 LHTAAREGHVTDTALLEKEASOACMKKKGGTPPLHV-AKYKGVRVLAELLEHDHPNAAG 570
F;661-693/Domain: ankyrin repeat homology <AN19>	: : : : : : : : : : : : : : : : : : :
F;694-726/Domain: ankyrin repeat homology <AN20>	Qy 67 PATLTPRVHDAAREGFLDYL-VVLRAGARLDYDAW-GRLPVDLAEELGHDRVARYL-- 122
F;727-759/Domain: ankyrin repeat homology <AN21>	: : : : : : : : : : : : : : : : : : :
F;760-792/Domain: ankyrin repeat homology <AN22>	Db 571 KNGLT-PLHYAVHHNNDIVKLPLPRGGs- -PHSPAWNCTPLHIAKQNOIEVARSLLQ 627
F;793-825/Domain: ankyrin repeat homology <AN23>	: : : : : : : : : : : : : : : : : : :
Query Match 20.8%; Score 158; DB 2; Length 3924;	Qy 123 ---RRAAGCTGSNHNARIDAEEGPSDI 146
Best Local Similarity 37.3%; Pred. No. 2.1e-06;	Db 628 YGGSANAESYGVTPPLHAAQEGETEM 654
Matches 48; Conservative 18; Mismatches 59; Indels 4; Gaps 3;	Db 629 YGGSANAESYGVTPPLHAAQEGETEM 654
RESULT 13	Db 630 YGGSANAESYGVTPPLHAAQEGETEM 654
Qy 8 LATAAARGRVEEVRALEAVALPNAPNSYGRPPIQV-MMMGSARVAELLLLHGAEPNCA 66	Db 631 YGGSANAESYGVTPPLHAAQEGETEM 654
Db 468 LHMAAARGOEVVRCLRLNGALYDARAEEQTPHTASRIGKTETIVQLLOMHPANT 527	Db 632 YGGSANAESYGVTPPLHAAQEGETEM 654
Qy 67 PATLTPRVHDAAREGFLDYL-VVLRAGARLDYDAW-GRLPVDLAEELGHDRVARYL-- RA 124	Db 633 YGGSANAESYGVTPPLHAAQEGETEM 654
: : : : : : : : : : : : : : : : : : :	Db 634 YGGSANAESYGVTPPLHAAQEGETEM 654
Db 528 TNGYT PLHTSAREGQDVDSVLLERAKHSLATKKGFTPLHVAKTKGSLDVAKLILLQR 586	Db 635 YGGSANAESYGVTPPLHAAQEGETEM 654
Qy 125 AAGGTGSN 133	Db 636 YGGSANAESYGVTPPLHAAQEGETEM 654
: : : : : : : : : : : : : : : : : : :	Db 637 YGGSANAESYGVTPPLHAAQEGETEM 654
Db 587 AAADSAKKN 595	Db 638 YGGSANAESYGVTPPLHAAQEGETEM 654
RESULT 12	Db 639 YGGSANAESYGVTPPLHAAQEGETEM 654
S3771 ankyrin, erythrocyte - mouse	Db 640 YGGSANAESYGVTPPLHAAQEGETEM 654
C;Species: Mus musculus (house mouse)	Db 641 YGGSANAESYGVTPPLHAAQEGETEM 654
C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999	Db 642 YGGSANAESYGVTPPLHAAQEGETEM 654
C;Accession: S37771	Db 643 YGGSANAESYGVTPPLHAAQEGETEM 654
R;Birkemeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.	Db 644 YGGSANAESYGVTPPLHAAQEGETEM 654
J. Biol. Chem. 268, 9533-9540, 1993	Db 645 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found among the mRNAs for the ankyrin genes. S37771; MUID:93252825	Db 646 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Reference number: S37771	Db 647 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Status: preliminary	Db 648 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Molecule type: mRNA	Db 649 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Residues: 1-1848 <1LR>	Db 650 YGGSANAESYGVTPPLHAAQEGETEM 654
A;Cross references: EMBL:X69063; PIDN:CAA48801.1; PIDN:g311816; PIDN:g311817	Db 651 YGGSANAESYGVTPPLHAAQEGETEM 654
C;Superfamily: ankyrin; ankyrin repeat homology	Db 652 YGGSANAESYGVTPPLHAAQEGETEM 654
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F;114-146/Domain: ankyrin repeat homology <AN03>	Db 657 YGGSANAESYGVTPPLHAAQEGETEM 654
F;147-175/Domain: ankyrin repeat homology <AN04>	Db 658 YGGSANAESYGVTPPLHAAQEGETEM 654
F;176-208/Domain: ankyrin repeat homology <AN05>	Db 659 YGGSANAESYGVTPPLHAAQEGETEM 654
F;209-241/Domain: ankyrin repeat homology <AN06>	Db 660 YGGSANAESYGVTPPLHAAQEGETEM 654
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F;276-307/Domain: ankyrin repeat homology <AN08>	Db 662 YGGSANAESYGVTPPLHAAQEGETEM 654
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F;374-406/Domain: ankyrin repeat homology <AN11>	Db 665 YGGSANAESYGVTPPLHAAQEGETEM 654
F;407-439/Domain: ankyrin repeat homology <AN12>	Db 666 YGGSANAESYGVTPPLHAAQEGETEM 654
F;430-472/Domain: ankyrin repeat homology <AN13>	Db 667 YGGSANAESYGVTPPLHAAQEGETEM 654
F;473-505/Domain: ankyrin repeat homology <AN14>	Db 668 YGGSANAESYGVTPPLHAAQEGETEM 654
F;506-538/Domain: ankyrin repeat homology <AN15>	Db 669 YGGSANAESYGVTPPLHAAQEGETEM 654
F;539-571/Domain: ankyrin repeat homology <AN16>	Db 670 YGGSANAESYGVTPPLHAAQEGETEM 654
F;572-604/Domain: ankyrin repeat homology <AN17>	Db 671 YGGSANAESYGVTPPLHAAQEGETEM 654
F;605-631/Domain: ankyrin repeat homology <AN18>	Db 672 YGGSANAESYGVTPPLHAAQEGETEM 654
F;638-670/Domain: ankyrin repeat homology <AN19>	Db 673 YGGSANAESYGVTPPLHAAQEGETEM 654
F;671-703/Domain: ankyrin repeat homology <AN20>	Db 674 YGGSANAESYGVTPPLHAAQEGETEM 654
F;704-736/Domain: ankyrin repeat homology <AN21>	Db 675 YGGSANAESYGVTPPLHAAQEGETEM 654
F;737-769/Domain: ankyrin repeat homology <AN22>	Db 676 YGGSANAESYGVTPPLHAAQEGETEM 654
F;770-802/Domain: ankyrin repeat homology <AN23>	Db 677 YGGSANAESYGVTPPLHAAQEGETEM 654
Query Match 18.1%; Score 137.5; DB 2; Length 1848;	Qy 123 ---RRAAGCTGSNHNARIDAEEGPSDI 146
Best Local Similarity 34.7%; Pred. No. 8e-05;	Db 678 YGGSANAESYGVTPPLHAAQEGETEM 646
Matches 51; Conservative 17; Mismatches 68; Indels 11; Gaps 6;	Db 679 YGGSANAESYGVTPPLHAAQEGETEM 646

RESULT 14 C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
 B35049 C:Accession: A35049
 ankyrin 1, erythrocyte splice form 3 - human
 N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A:Title: cDNA sequence for human erythrocyte ankyrin.
 A:Status: (man)
 A:Reference number: A35049; MUID:90175370
 A:Accession: B35049
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1856 <LAM>
 A:Cross-references: GDB:ANK1; ANK
 A:Gene: GDB:ANK1; ANK
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 C:Form 3 #status predicted <MAT>
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 F;2-1513-1676-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F;2-1513-1676-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F;2-1513-1676-1880/Domain: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;44-16/Domain: ankyrin repeat homology <AN02>
 F;77-109/Domain: ankyrin repeat homology <AN02>
 F;110-142/Domain: ankyrin repeat homology <AN03>
 F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN07>
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 F;502-534/Domain: ankyrin repeat homology <AN15>
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 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-799/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>
 F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match Score 17.6%; DB 2; Length 1856;
 Best Local Similarity 35.4%; Pred. No. 0.00019;
 Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

Qy 8 LATAAARGRVEEVRALEAVALPNAPNSYGRPQQV-MMAGSARVAELLHLGAEPNCAD 66
 Db 507 LHIAAREGHETVETVALLKEASQACMTKGFTPLHVAKYKGVRAELLERDHPNAAG 566

Query Match Score 17.6%; DB 2; Length 1880;
 Best Local Similarity 35.4%; Pred. No. 0.0002;
 Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

Qy 8 LATAAARGRVEEVRALEAVALPNAPNSYGRPQQV-MMAGSARVAELLHLGAEPNCAD 66
 Db 567 KNGIT-PLHVAVVHHNNLDIVKILLPRGS--PHSPAWNGTPHLIAAKQNQEVARSLIQ 623

Db 507 LHIAAREGHETVETVALLKEASQACMTKGFTPLHVAKYKGVRAELLERDHPNAAG 566

Qy 123 --RAAACGTRGSNHNHARIDAEGPSDI 146
 Db 624 YGGSANAESVQGVTPHLAAQEGHAE 650

RESULT 15
 A35049 ankyrin 1, erythrocyte splice form 2 - human
 N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)

Search completed: May 7, 2002, 12:33:45
 Job time: 120 sec

Scoring table:	BIOSUN62	Query	MEPSADWILATAAARGYBEEV.....TRGSNHARTDAEAGPSDIPD	Length	148	Description		ALIGNMENTS
Searched:	Gapop 10.0 , Gapext 0.5	Total number of hits satisfying chosen parameters:	100059	Minimum DB seq length:	0	RESULT 1		
Maximum DB seq length:	2000000000	Post-processing:	Minimum Match 0%	CDN2_HUMAN	1	CDN2_HUMAN	STANDARD;	PRT; 156 AA.
Database :	SwissProt_39;*	Maximum Match 10%	Listing first 45 summaries	ID	CDN2_HUMAN	AC	PA2771; Q15191;	PRT; 156 AA.
						DT	01-NOV-1995 (Rel. 32, Created)	
						DT	15-JUL-1998 (Rel. 36, Last sequence update)	
						DT	20-AUG-2001 (Rel. 40, Last annotation update)	
						DE	CYCLIN-DEPENDENT KINASE 4 (CDK4) (P16-INK4A) (P16-INK4)	
						DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1),	
						GN	CDKN2A OR CDKN2.	
						OS	Homo sapiens (Human).	
						OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
						OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
						OX	NCBI_TaxID=9606;	
						RN	[1]	
						RP	SEQUENCE FROM N.A.	
						RX	Medline-94081956; PubMed-8259215;	
						RA	Serrano M., Hannon G.J., Beach D.;	
						RA	"A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.";	
						RT	RT	
						RL	Nature 366:704-707(1993).	
						RN	[2]	
						RP	SEQUENCE OF 51-152 FROM N.A.	
						RX	Medline-9202645; PubMed-8153634;	
						RA	Kamb A., Grulis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,	
						RA	Tavriqian S.V., Stockert E., Day R.S., III, Johnson B.E.,	
						RA	Skolnick M.H.;	
						RT	"A cell cycle regulator potentially involved in genesis of many tumor types.";	
						RT	Science 264:436-440(1994).	
						RN	[3]	
						RP	SEQUENCE OF 1-20 FROM N.A.	
						RX	Medline-9618088; PubMed-8622687;	
						RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;	
						RA	"Regulation of p16CDKN expression and its implications for cell immortalization and senescence.";	
						RL	Mol. Cell. Biol. 16:859-867(1996).	
						RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.	
						RX	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;	
						RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor p16INK4a.";	
						RL	Nature 395:237-243(1998).	
						RN	[4]	
						RP	REVIEW ON MELANOMA VARIANTS.	
						RX	Medline-96377761; PubMed-8783570;	
						RA	Dracopoli N.C., Fountain J.W.;	
						RT	"CDKN2 mutations in melanoma.";	
						RL	Cancer Surv. 26:115-132(1996).	
						RN	[5]	
						RP	REVIEW ON VARIANTS.	
						RX	Medline-96303699; PubMed-8723678;	
						RA	Smith-Sorensen B., Hoving E.;	
						RT	"CDKN2 (P16INK4A) somatic and germline mutations.";	
						RL	Hum. Mutat. 7:294-303(1996).	

RN	[7] VARIANTANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).	Hum. Mol. Genet. 7:209-216(1998).
RP	"Mutants associated with familial melanoma impair p16INK4 function.";	Hum. Mol. Genet. 7:209-216(1998).
RA	VARIANTANTS MELANOMA PRO-24; ILE-53 AND C-107, AND VARIANTANTS V-68; T-85 AND T-148.	[16]
RA	VARIANTANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.	ERATUM.
RA	MEDLINE=9438355; PubMed=8060323;	Souffir N., Avril M.-F., Chompret A., Demenais F., Bomblé J., Demenais F., Bressac-De Paillerets B.;
RA	Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;	Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Paillerets B.;
RP	"Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41 (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small cell lung carcinomas.";	Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Paillerets B.;
RT	Biochem. Biophys. Res. Commun. 202:1426-1430(1994).	"Novel germline p16INK4 allele (Asp145Cys) in a family with multiple pancreatic carcinomas.";
RL	"Germline p16 mutations in familial melanoma.";	Var. Pancreatic Carcinoma CYS-146.
RN	Nat. Genet. 8:15-21(1994).	Modakaluk C.A., Hruban R.H., Lieberman A., Smyrk T., Fusaro L., RA
RP	VARIANTANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.	Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.; RT
RX	MEDLINE=95078916; PubMed=9878787;	"Novel germline p16INK4 allele (Asp145Cys) in a family with multiple pancreatic carcinomas.";
RA	Zhou X., Tarnan L., Yin J., Jiang H.-Y., Suzuki H., Ryu M.-G.,	RT
RA	Abraham J.M., Meltzer S.J.;	RT
RA	"The MTS1 gene is frequently mutated in primary human esophageal tumors.";	RT
RT	RT	Regulator of the proliferation with CDK4 or CDK6.
RT	Oncogene 9:3737-3741(1994).	-1 - SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
RN	[10]	-1 - DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A WIDE RANGE OF TISSUES.
RP	VARIANTANTS	-1 - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.
RX	Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shieki M., Zarifiwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;	CC
RA	"Mutations in the p16INK4/MtSL1/CDKN2, p15INK4B/MtS2, and p18 genes in primary and metastatic lung cancer.";	CC
RA	Cancer Res. 55:1448-1451(1995).	CC
RN	VARIANTANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.	CC
RP	CHARACTERIZATION OF VAR. "T-49; S-71; L-81; P-87; W-101; D-126 & T-148.	CC
RX	MEDLINE=95121500; PubMed=8595405;	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M., Haluska F.G., Dracopoli N.C., Hayward N.K., Fountaine J.W., Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D., Dracopoli N.C.;	CC
RT	"Mutations of the CDKN2/p16INK4 gene in Australian melanoma kindreds.";	CC
RL	Hum. Mol. Genet. 4:1845-1852(1995).	CC
RN	CHARACTERIZATION OF VAR. "T-49; S-71; L-81; P-87; W-101; D-126 & T-148.	CC
RP	Rapade K., Hussussian C.J., Sikorski R.S., Varmus H.E., Glendening J.M., Dracopoli N.C., Serrano M., Hannon G.J., Beach D., Dracopoli N.C.;	CC
RA	"Mutations associated with familial melanoma impair p16INK4 function.";	CC
RA	Nat. Genet. 10:114-116(1995).	CC
RN	VARIANTANTS MELANOMA I-53 AND C-107, AND VARIANTANTS V-68; T-85 AND T-148.	CC
RP	"Mutants associated with familial melanoma impair p16INK4 function.";	CC
RA	VARIANTANTS MELANOMA PRO-24; ILE-53 AND C-107, AND VARIANTANTS V-68; T-85 AND T-148.	CC
RA	Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J., Lucohina L.C., Unsai H., O'Neill E., Koh J., Finkelstein D.M., Isseibacher K.J., Sober A.J., Haber D.A.	CC
RA	"Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in familial melanoma: analysis of a clinic-based population.";	CC
RT	Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).	CC
RL	MEDLINE=9632359; PubMed=8710906;	CC
RA	Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J., Lucohina L.C., Unsai H., O'Neill E., Koh J., Finkelstein D.M., Isseibacher K.J., Sober A.J., Haber D.A.	CC
RA	"Germline mutations of the CDKN2 gene in UK melanoma families.";	CC
RA	Bishop D.T., Bishop J.N., Bataille V., Peters G., Cuzick J., Selby P., Frischauft A.-M., Harland M., Melton R., Gruij N., Pinney E., Brookes S., Spurr N.K.,	CC
RA	"Germline mutations of the CDKN2 gene in UK melanoma families.";	CC
RA	Hum. Mol. Genet. 6:2061-2067(1997).	CC
RN	VARIANTANTS FAMILIAL MELANOMA.	[15]
RP	MEDLINE=98087572; PubMed=9425228;	Souffir N., Avril M.-F., Chompret A., Demenais F., Bomblé J., Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Paillerets B.;
RA	"Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";	Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Paillerets B.;
RT	"Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone families in France.";	E > D (IN A BILARY TRACT TUMOR). /FTId=VAR_001415.

Query Match	Score 753; DB 1; Length 156;
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0; Gaps	0;
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Y	EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVRLPVLDAELGLRDYAR 120
D	EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVRLPVLDAELGLRDYAR 128
Y	YLRAAAGGTRGSNHARTDAAGCPSDIPD 148
b	YLRAAAGGTRGSNHARTDAAGCPSDIPD 156
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P55271;	PRT;
01-OCT-1996 (Rel. 34, Created)	130 AA.
01-OCT-1996 (Rel. 34, Last sequence update)	
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) .	
CDKN2B.	
Mus musculus (Mouse).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]	
REB1_PAXID=10090.	
SEQUENCE FROM N.A. MEDLINE=95380169; PubMed=7651726;	
Queille D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine p16INK4a and p15INK4b genes."; Oncogene 11:1635-645(1995).	
SEQUENCE FROM N.A. STRAIN=C57BL/6J X DBA; MEDLINE=9732247 X [2]	
Malumbres M., de Castro I., Santos J., Melendez B., Mangues R., Serrano M., Pellicer A., Fernandez-Piqueras J.; "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by deletion and de novo methylation with independence of p16INK4a alterations in murine primary T-cell lymphomas."; Oncogene 14:1361-1370(1997).	
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY SIMILARITY).	
SUBUNIT: HETERO DIMER OF CDK4 WITH CDK6. POTENT INHIBITOR.	
- - - TISSUE SPECIFICITY: EXPRESSED Ubiquitously.	
- - - INDUCTION: BY TGF-BETA.	
- - - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.	
- - - SIMILARITY: CONTAINS 4 ANK REPEATS.	
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EMBL; U66085; AAB9833.1; JOINED.	
R MGD; MGI:104737; Cdkn2b.	
R InterPro; IPR02110; ANK.	
R Pfam; PF00023; ank; 3.	
R SMART; SM00248; ANK_REPEAT; 1.	
PROSITE; PS50397; ANK_REPEAT_REGION; 1.	
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.	
FT REPEAT 5 34 ANK 1.	
FT REPEAT 38 66 ANK 2.	
FT REPEAT 71 100 ANK 3.	
FT REPEAT 104 130 ANK 4.	
SQ SEQUENCE 130 AA; 1378 MW; 7AAD60FF552CF9 CRC64;	
Query Match 69.6%; Score 529; DB 1; Length 130;	
Best Local Similarity 88.3%; Pred. No. 1.5e-44;	
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;	
Y 8 LATAAARGRVEEVRAALPVNAPNSYGRPIQVMMGSSARVAELLHGAEPNCADP 67	
Db 10 LATAAARGGVEEVQLEGGADPVALNRGRPPIQVMMGSSAQAEVLLHGAEPNCADP 69	
QY 68 ATLIRPVHDAAREGFLDTLVLRAGARDVRLPVLDAELGLRDYARLRAAG 127	
Db 70 ATLIRPVHDAAREGFLDTLVLRAGARDVRLPVLDAEQQHGRDIARYLHAATG 129	
RESULT 3	
CDN5_RAT	STANDARD;
ID CDN5_RAT	PRT;
AC P55272;	130 AA.
DT 01-OCT-1996 (Rel. 34, Created)	
DT 01-OCT-1996 (Rel. 34, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).	
DN CDKN2B OR INKA.	
OS Ratmus norvegicus (Rat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]	
NCBI_Taxid=10116;	
RN SEQUENCE FROM N.A. MEDLINE=96013392; PubMed=7546221;	
RX Hino O., Kobayashi E., Hirayama Y., Kubo Y., RA Tsuchiya H., Kikuchi Y., Mitani H.; "Molecular genetic basis of renal carcinogenesis in the Eker rat model. Carcinog. 14:23-27(1995).	
RN [2]	
RN SEQUENCE OF 46-86 FROM N.A. MEDLINE=95228016; PubMed=7712460;	
RX Knapik D.F., Serrano M., Beach D., Trono D., Walker C.L.; RA RT "Association of rat p15INK4B/p16INK4A deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors."; Cancer Res. 55:1607-1612(1995).	
CC - - - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.	
CC - - - SUBUNIT: HETERO DIMER OF TGF-BETA INDUCED CELL CYCLE ARREST (BY SIMILARITY).	
CC - - - TISSUE SPECIFICITY: EXPRESSED Ubiquitously.	
CC - - - INDUCTION: BY TGF-BETA.	
CC - - - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.	
CC - - - SIMILARITY: CONTAINS 4 ANK REPEATS.	
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EMBL; U66085; AAB9833.1; JOINED.	
R MGD; MGI:104737; Cdkn2b.	
R InterPro; IPR02110; ANK.	
R Pfam; PF00023; ank; 3.	
R SMART; SM00248; ANK_REPEAT; 1.	
PROSITE; PS50398; ANK_REPEAT; 1.	
DR EMBL; S79750; AAB35360; 1.	
DR EMBL; S77734; NOT_ANNOTATED_CDS.	

DR	InterPro; IPR002110; ANK.	RA	Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Xiong Y., Beach D.H., Yokota J., Harris C.C.; "Mutations in the P16INK4A/MTS1/CDKN2, P15INK4B/MTS2, and p18 genes in primary and metastatic lung cancer." RT
DR	SMART; SM00248; ANK; 3.	RA	Cancer Res. 55:1448-1451(1995).
DR	PROSITE; PS50088; ANK_REPEAT; 1.	RL	-1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
DR	PROSITE; PS50295; ANK REP REGION; 1.	CC	-1- SUBUNIT: HETEROODIMER OF P14 WITH CDK4.
KW	Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.	CC	-1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION, LONG ISOFORM.
CELL CHAIN	1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,	CC	-1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.
FT	CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,	CC	-1- SIMILARITY: CONTAINS 2 ANK REPEATS.
FT	INIT_MET 46 46 SHORT ISOFORM.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.iss-sib.ch/announce/ or send an email to license@iss-sib.ch).
FT	REPEAT 5 34 FOR SHORT ISOFORM.	CC	-----
FT	REPEAT 38 66 ANK 1.	CC	-----
FT	REPEAT 71 100 ANK 2.	CC	-----
FT	REPEAT 104 130 ANK 3.	CC	-----
SEQUENCE	130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;	CC	-----
Query Match	68.9%; Score 524; DB 1; Length 130;	CC	-----
Best Local Similarity	86.7%; Pred. No. 4.5e-44;	CC	-----
Matches	104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;	CC	-----
Qy	8 LATAAARGRVEVRALEAVLPNAPNSYGRPPIQMMGCSRVAEFLLLHGAEPNCADP	DR	U17075; AAC50075; 1; -;
Db	10 LATAAARGQVETVRQLEAGDPNAVNRGGRPPIQYMMGCSRVAEFLLLHGAEPNCADP	DR	EMBL; L36844; AAA50282; 1; -;
Qy	68 ATLTRPYHDAAAREGFDLTLYLHRAGARDLVCDANGRLPVDAEEGHDRVARYLRAAG	DR	EMBL; S68805; AAD14049; 1; -;
Db	70 ATLTRPYHDAAAREGFDLTLYLHRAGARDLVCDANGRLPVDAEEGHDRVARYLRAAG	DR	MIM; 600431; -;
RESULT	4	InterPro; IPR002110; ANK.	
ID	CDN5_HUMAN STANDARD; PRT; 138 AA.	DR	Pfam; PF00023; 1; ank; 3
AC	P42772; PRT; 138 AA.	DR	PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
DT	01-NOV-1995 (Rel. 32, Created)	DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DT	01-NOV-1995 (Rel. 32, Last sequence update)	DR	Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.
DT	20-AUG-2001 (Rel. 40, Last annotation update)	FT	39 1 (INCOMPLETE).
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B) (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).	FT	REPEAT 73 103 ANK 2.
GN	CDKN2B OR MTS2.	FT	G > E (IN LUNG ADENOCARCINOMA).
OS	Homo sapiens (Human).	FT	/FTid=VAR_001488.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	FT	A > V (IN LUNG ADENOCARCINOMA).
NCBI_TAXID	9606; [1]	VARIANT	/FTid=VAR_001489.
RN	SEQUENCE FROM N.A. RP SEQUENCE OF 53-138 FROM N.A. MEDLINE-95095079; PubMed=8001816; RX Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L., Matera G.A., Xiong Y., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., RT "Growth suppression by p18, a p16INK4a/MTS1- and p14INK4B/MTS2-related CDKN2 inhibitor, correlates with wild-type PRB function.", RT Genes Dev. 8:2939-2952(1994). RL [2]	Qy	SADWIAAARGRVEVRALEAVLPNAPNSYGRPPIQMMGCSRVAEFLLLHGAEPN 63
RN	SEQUENCE FROM N.A. RP SEQUENCE OF 53-138 FROM N.A. MEDLINE-94359613; PubMed=8078588; RX Hannon G.J., Beach D.; "p15INK4B is a potent effector of TGF-beta-induced cell cycle arrest.", RT Nature 371:257-261(1994).	Db	14 SDEGLASAAARGLVEVRALEAVLPNAPNSYGRPPIQMMGCSRVAEFLLLHGAEPN 73
RN	SEQUENCE FROM N.A. RP SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	Qy	64 CADPATLTREPVHDAAREGFDLTLYLHRAGARDLVCDANGRLPVDAEEGHDRVARYL 123
RN	SEQUENCE FROM N.A. RP SEQUENCE OF 53-138 FROM N.A. MEDLINE-94359613; PubMed=8078588; RX Hannon G.J., Beach D.; "p15INK4B is a potent effector of TGF-beta-induced cell cycle arrest.", RT Nature 371:257-261(1994).	Db	74 CADPATLTREPVHDAAREGFDLTLYLHRAGARDLVCDANGRLPVDAEEGHDRVARYL 133
RN	SEQUENCE FROM N.A. RP SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	RESULT	5
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	CDN2_MOUSE	STANDARD; PRT; 167 AA.
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	CDN2_MOUSE	STANDARD; PRT; 167 AA.
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	AC	P51480; 01-OCT-1996 (Rel. 34, Created)
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	DT	01-OCT-1996 (Rel. 34, Last sequence update)
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	DE	20-AUG-2001 (Rel. 40, Last annotation update)
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	GN	CDKN2A OR P16INK4A.
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	OS	Mus musculus (Mouse).
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	OX	NCBI_TaxID=10090;
RN	SEQUENCE OF 53-138 FROM N.A. MEDLINE-94204645; PubMed=8153634; RX Kamb A., Grulis N.A., Weaver-Felthaus J., Liu Q., Harshman K., Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., Skolnick M.H.; "A cell cycle regulator potentially involved in genesis of many tumor types.", RT Genes Dev. 8:2939-2952(1994). RL [2]	RN	[1]

SEQUENCE FROM N.A. MEDLINE=93380169; PubMed=7651726;

RP OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.

RX RN NCBI_TaxID=13616;

RA RP SEQUENCE FROM N.A.

RA RA Sherburn T.E., Gale J.M., Ley R.D.;

RA RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

RT CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).

RL CC -!- SUBUNIT: HETERO-DIMER WITH CDK4 OR CDK6 (BY SIMILARITY).

CC CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

CC CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.

CC CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.

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CC DR EMBL; AF06106; AAC23669.1; .

CC DR AF064808; AAC23670.1; .

CC DR InterPro; IPR002110; ANK.

CC DR Pfam; PF00023; ank; 3.

CC DR PROSITE; PS50088; ANK_REPEAT; 1.

CC DR PROSITE; PS50297; ANK REP REGION; 1.

CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; CYCLIN-DEPENDENT KINASE 4 INHIBITOR A, LONG ISOFORM.

CC FT CHAIN 1 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A, LONG ISOFORM.

CC FT CHAIN 35 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A, SHORT ISOFORM.

CC FT INIT-MET 35 35 FOR SHORT ISOFORM.

CC FT REPEAT 45 74 ANK 1.

CC FT REPEAT 78 106 ANK 2.

CC FT REPEAT 111 140 ANK 3.

CC SQ SEQUENCE 171 AA: 18707 MW: 694264F5D04F6CC CRC64;

Query Match Score 53.7%; Length 171;

Best Local Similarity 69.2%; Pred No. 1..1e-32;

Matches 83; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

Qy 4 QADNLATAAARGVEEVRAVALLAEAVALPNAPNSYGRPTIQVMGMSARVAELLHLGAEPN 63

Db 46 SGEKLTAAARGVEEVTEELGTNPNAVRGRSAIQVMGMGNVTLAQLQGPEN 105

Qy 64 CADPATLTPVHDAREGFLDTLVLRAGARDYDRAWGRLPYDIAELGHDRVARYARL 123

Db 106 TPDPTITLTPVHDAREGFLDTLMRLLRAGARDVLRDQGLPVLDAEQGHLVYAVYL 165

RESULT 7

CDN7_HUMAN STANDARD; PRT: 166 AA.

ID CDN7_HUMAN STANDARD;

ID AC F55273; Q13102;

AC DT 01-OCT-1996 (Rel. 34, Created)

AC DT 01-OCT-1996 (Rel. 34, Last sequence update)

AC DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).

GN GN CDKN2D.

OS Homo sapiens (Human).

OC OC Bovavirus; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

OC OC Mammalia; Eutheria; Primates; Catarrhini; Homino.

NCBI_TaxID=9606;

RP RP SEQUENCE FROM N.A.

RC RC TISSUE=Bone marrow.

RX RX MEDLINE=96121373; PubMed=8575754;

RA RA Okuda T., Hirai H., Valentine V.A., Shurtliff S.A., Kidd V.J.,

Euayranya; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

OS OS Monodelphis domestica (Short-tailed grey opossum).

OC OC

RA Lahti J.M., Sherr C.J., Downing J.R.;
RT "Molecular cloning, expression pattern, and chromosomal localization
of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases.";
RL Genomics 29:623-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96362662; PubMed=8741839;
RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
RA Zariali A.M., Mavera A.G., Xiong Y.;
RA "Isolation and characterization of p19INK4d, a p16-related inhibitor
specific to CDK6 and CDK4";
RL Mol. Biol. Cell 7:57-70(1996).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE="THYMUS";
RX MEDLINE=95257949; PubMed=7739548;
RA Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
Bishop D.T.;
RA "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";
RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
RX MEDLINE=98421670; PubMed=9751050;
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
RA "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
by the tumour suppressor p16INK4a.";
RT Nature 395:237-243(1998).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=8845510; PubMed=9782052;
RA Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
RA Holak T.A.;
RA "Structure of human cyclin-dependent kinase inhibitor p19(INK4d);
RT comparison to known ankyrin-repeat-containing structures and
RT implications for the dysfunction of tumor suppressor p16(INK4a)." ;
RT Structure 6:1279-1290(1998).
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC -!- INHIBITORS: CONTAINS 4 ANK REPEATS.
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CC -----
DR EMBL: U43399; AAB03772; 1; -.
DR EMBL: U40343; AAB1139; 1; -.
DR EMBL: U20498; AAB85436; 1; -.
DR EMBL: AF061327; AAC27450; 1; -.
DR PDB: 1N18; 16-FEB-99.
DR PDB: 1BDB; 14-OCT-98.
DR MIM: 600927; -.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50397; ANK_REPEAT_REGION; 1.
KW Cell cycle: Anti-oncogene; Repeat; ANK repeat; 3D-structure.
FT REPEAT 41 69 ANK 1.
FT REPEAT 73 102 ANK 2.
FT REPEAT 106 135 ANK 3.
FT REPEAT 138 166 ANK 4.

FT CONFLICT 159 159 AA; 17700 MW; Q > P (IN REF. 3).
SQ SEQUENCE 166 AA; 17700 MW; 2FACD11CF56340DC CRC64;
Query Match Score 259; DB 1; Length 166;
Best Local Similarity 44.0%; Pred. No. 2.7e-18;
Matches 66; Conservative 18; Mismatches 60; Indels 6; Gaps 3;
QY 4 SADMILATAARGRVEEVALL-PAVALDENAPNSYGRPPIQVMMGMSARVAELLILLGAEP 62
Db 8 AGDRLSGAAARGDVQEVRLLHRELVHDALNEFGKTALQVNMEGSTIALELLKGASAP 67
QY 63 NCADPATLTTRPVHDAAARGFLDTLVVLAGRDVRAWRGPFLVDAELGHDRVARYL 122
Db 68 NVQDTSG-TSPVHAAARGFLDTLVVLAGDYNVPDGTGALPHTLVQEGHTAVVSL 126
QY 123 RAAAG---GTRGSNHRIDAABGPSDIPD 148
Db 127 AAESDLHRRDARGLTPLLELALQRGQAODIVD 156

RESULT 8
CDN7_MOUSE STANDARD PRT;
ID CDN7_MOUSE STANDARD PRT;
ID 060773; Q60794;
AC 060773; Q60794;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RN TRAIN=C57BL_KAP10;
RX MEDLINE=9557948; PubMed=7739547;
RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
RT "Novel INKA-proteins, p19 and p18, are specific inhibitors of the
cyclin D-dependent kinases CDK4 and CDK6.";
RT Mol. Cell. Biol. 15:2672-2681(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9257949; PubMed=7739548;
RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
RT "Identification of human and mouse p19, a novel CDK4 and CDK6
inhibitor with homology to p16INK4a.";
RT Mol. Cell. Biol. 15:2682-2688(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=98013176; PubMed=9353127;
RA Luh F.Y., Archer S.J., Donaile P.J., Smith B.O., Owen D., Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
RA Laue E.D.;
RT Structure of the cyclin-dependent kinase inhibitor p19Ink4d.";
RT Nature 389:999-1003(1997).
RL 15:2682-2688(1995).
RN [4]
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC -!- INHIBITORS: CONTAINS 3 ANK REPEATS.
CC -----
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CC -----
CC DR EMBL: U19597; AAC52194; 1.
CC DR EMBL: U20497; AAA85437; 1.
CC DR PDB: 1AP7; 16-SEP-98.

MGD; MGI:105387; Cdkn2d.	DR SMART; SMO0248; ANK; 2.
InterPro; IPR002110; ANK.	DR PROSITE; PS50088; ANK_REPEAT; 2.
Pfam; PF00023; ank; 3.	DR PROSITE; PS50297; ANK_REPEAT; 1.
SMART; SM00268; ANK; 1.	KW Cell cycle; Repeat; ANK repeat.
PROSITE; PS50297; ANK_REPEAT; 1.	FT REPEAT 4 33 ANK 1.
PROSITE; PS50088; ANK repeat;	FT REPEAT 37 65 ANK 2.
Cell cycle; Anti-oncogene; Repeat; ANK repeat.	FT REPEAT 69 98 ANK 3.
REPEAT 73 ANK 1.	FT REPEAT 102 132 ANK 4.
REPEAT 106 135 ANK 2.	FT REPEAT 136 165 ANK 5.
REPEAT 138 166 ANK 3.	SQ SEQUENCE 168 AA; 18056 MW; BC88D5489307E128 CRC64;
SEQUENCE 166 AA; 17894 MW; 9E745C23B7EB22 CRC64;	Query Match 30 5%; Score 231 5%; DB 1; Length 168; Best Local Similarity 40 3%; Pred. No. 1.3e-15; Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;
Query Match 32.8%; Score 24 9; DB 1; Length 166; Best Local Similarity 44 38; Pred. No. 2.5e-17; Matches 70; Conservative 18; Mismatches 52; Indels 18; Gaps 5;	Qy 2 EPSADMVLAAARGVEYVALLAVALLNAPNSYGRPIQVMMGMSARVAELLLLHGA 61 Db 3 EPWGNEELASAARGGLEQTSLLQNQNNVNTAQNGFGRTAQLVNLGNPPIARRLRLGAN 62
6 DVIATATAARGVEYVALL- EYVALWAPNSYGRPIQVMMGMSARVAELLLLHGAEPNC 64	Qy 62 PNCADPATLTPVHDAAREGFLDTLVLAHAGARDLVRDAWGRPLVDLAEGLHRDVARY 121 Db 63 PNLKD-GTGFAVIHDAAREGFLDQVALLEQFQADVNIDNEGNEULPLHLAKEGLHPVVF 121
10 DRISGARSHDQEVRRLHRELVPALNRKGKTAQVMMGSPAVALELKQGASPNV 69	Qy 122 LRAAGGTROSNSNHARIDA 140 Db 122 LMKHTACNVGHRNKGDTA 140
65 ADPATLTPVHDAAREGFLDTLVLAHAGARDLVRDAWGRPLVDLAEGLHRDVARYL- 122	RESULT 10
70 QD-ASGTSPVHDARTGFLDTKVVLAREGHSSSVVSFLAP 128	CDDN6_HUMAN STANDARD; PRT; 168 AA.
123 ---R-SAAAGT--- -RSNHNARIDAEGPSDIP 147	ID CDDN6_HUMAN STANDARD; PRT; 168 AA.
129 ESDLHHRDASGLPLEALARQSQAQNLM-DILQGHMMTP 165	AC P42773; Created)
CDN6_MOUSE STANDARD; PRT; 168 AA.	DT 01-NOV-1995 (Rel. 32, Last sequence update)
CDN6_MOUSE STANDARD; PRT; 168 AA.	DT 01-NOV-1995 (Rel. 32, Last annotation update)
CDN6_MOUSE STANDARD; PRT; 168 AA.	DT 20-AUG-2001 (Rel. 40, Last annotation update)
CDN6_MOUSE STANDARD; PRT; 168 AA.	DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).
CDN6_MOUSE STANDARD; PRT; 168 AA.	DE CDKN2C OR CDKN6
CDN6_MOUSE STANDARD; PRT; 168 AA.	GN Homo sapiens (Human).
CDN6_MOUSE STANDARD; PRT; 168 AA.	OS Bovaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OC NCBI_TAXID=9606;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RX SEQUENCE FROM N.A. [1]
CDN6_MOUSE STANDARD; PRT; 168 AA.	RX MEDLINE=95095079; PubMed=8001816;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L., RA Matera G.A., Xiong Y.; RA "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; RA Matera G.A., Xiong Y.; RA "Structure of the gene encoding the human cyclin-dependent kinase p18 and mutation analysis in breast cancer cells"; RA Biochem. Biophys. Res. Commun. 247:146-153 (1996). RA TISSUE-Breast; RX MEDLINE=98300299; PubMed=9636670;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.; RA "Structure of the gene encoding the human cyclin-dependent kinase p18 mutant defective in CDK6 binding in human breast cancer cells"; RA Biochem. Biophys. Res. Commun. 247:146-153 (1996). RA TISSUE-Breast; RX MEDLINE=96138606; PubMed=8840966;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA Lapointe J., Lachance Y., Labrie Y., Labrie C.; RA "A p18 mutant defective in CDK6 binding in human breast cancer cells"; RA Biochem. Biophys. Res. Commun. 247:146-153 (1996). RA TISSUE-Breast; RX MEDLINE=98300299; PubMed=9636670;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA Venkataraman R., Swaminathan K., Marmorstein R.; RA "Crystal structure of the CDK4/6 inhibitory protein p18INK4C provides insights into ankyrin-like repeat structure/function and tumor-derived p16INK4 mutations.";
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS). RX MEDLINE=98100086; PubMed=9437433;
CDN6_MOUSE STANDARD; PRT; 168 AA.	RA InterPro; IPR002110; ANK.
CDN6_MOUSE STANDARD; PRT; 168 AA.	RG Pfam; PF00023; ank; 4.
SEQUENCE FROM N.A.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See license@isb-sib.ch).
STRAIN=C57BL/KAP/AN;	EMBL; U19596; AAC52193.1; -.
MEDLINE=95257948; PubMed=7719547;	MGD; MGI:105388; Cdkn2c.
Hirai H., Rousset M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;	InterPro; IPR002110; ANK.
"Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.";	Pfam; PF00023; ank; 4.
Mol. Cell. Biol. 15:2672-2681(1995).	
-1 FUNCTION: INTERACTS STRONGLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDODERMOGENOUS RETINOBLASTOMA PROTEIN RB.	
-1 SUBUNIT: HETERO DIMER OF P18 WITH CDK6 (BY SIMILARITY).	
-1 SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.	
-1 SIMILARITY: CONTAINS 5 ANK REPEATS.	
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C	EMBL; U19596; AAC52193.1; -.
C	MGD; MGI:105388; Cdkn2c.
C	InterPro; IPR002110; ANK.
C	Pfam; PF00023; ank; 4.

RL	Nat. Struct. Biol. 5:74-81(1998). [5]	DT 01-APR-1993 (Rel. 25, Created) DT 01-OCT-1996 (Rel. 34, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update)
RP	STRUCTURE BY NMR. MEDLINE=9917508;	DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
RX	LI J., Byeon I.-J.L., Erickson K., Poi M.-J., O'Maille P., Selby T., RA Tsai M.-D.;	GN Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. NCBI_TaxID=9606;
RT	"Tumor suppressor INK4: determination of the solution structure of loops in p18INK4C and demonstration of the functional significance of loops in p18INK4C and p18INK4A."	OX [1] RN SEQUENCE FROM N.A. (ISOFORM 1). RN SEQUENCE FROM N.A. (ISOFORM 1). RC TISSUE=Brain stem; MEDLINE=94075409; PubMed=8253844;
RT	Blochinger 38:2930-2940(1999). -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGENOUS RETINOBLASTOMA PROTEIN RB.	RA Chan W., Kordali E., Bennett V.; "440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons."; RT RT domain. RL J. Cell Biol. 123:1463-1473(1993).
CC	-1- SUBUNIT: HETEROODIMER OF P18 WITH CDK6.	RN [2] RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). RX TISSUE=Brain stem; PubMed=1830053;
CC	-1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO FOUND IN PANCREAS AND HEART.	RA Otto E., Kunimoto M., McLaughlin T., Bennett V.; "Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes."; RT RT [3] RL J. Cell Biol. 114:241-253(1991).
CC	-1- DISEASE: CDKN2 MUTATIONS ARE INVOLVED IN TUMOR FORMATION.	RN [4] RN Submitted (MAY-1999) to the EMBL/CenBank/DBDBJ databases.
CC	-1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.	RA Carpenter S.; RL Submitted (MAY-1999) to the EMBL/CenBank/DBDBJ databases.
CC	-1- SIMILARITY: CONTAINS 4 ANK REPEATS.	RN [4] RN SEQUENCE OF 463-495 FROM N.A. RX MEDLINE=92009921; PubMed=1833108; RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E., Lux S.E., Ward D.C., Forrest B.G.; "Isolation and chromosomal localization of a novel nonerythroid ankyrin gene."; RT RT Genomics 10:858-866(1991).
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	CC CC FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-SKELETAL ELEMENTS; THEY BIND TO THE ERTHROCYTE MEMBRANE PROTEIN GP85, BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETON PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. ERTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CITOPLASMIC DOMAIN OF THE ERTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC	CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPlicing.	CC CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROUGHOUT THE BRAIN.
DR	EMBL; U17074; AAC50074.1; -.	CC CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE AND FUNCTION (POTENTIAL).
DR	EMBL; AF041248; AAC39782.1; -.	CC CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
DR	EMBL; AF041250; AAC39783.1; -.	CC CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR	EMBL; AF041249; AAC39783.1; JOINED.	CC CC
PDB	1IHB: 13-JAN-99.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
PDB	1B09: 13-SEP-99.	CC DR EMBL; X56957; CAA40278.1; -.
MIM	603369; -.	CC DR EMBL; X56958; CA40279.2; -.
DR	InterPro: IPR002110; ANK_Pfan; PF00023; ank; 4.	CC DR EMBL; M37123; AAA62828.1; -.
DR	SMART: SM00248; ANK; 2.	CC PIR; S14533; S14533.
DR	PROSITE: PS50088; ANK_REPEAT; 2.	CC DR PIR; A39633; A39643.
DR	PROSITE: PS50297; ANK_REPEAT; 1.	CC PIR; B31643; B31643.
KW	Cell cycle; Repeat; ANK repeat; Disease mutation; 3D-structure.	CC DR PIR; S14569; S14569.
FT	REPEAT 4 33 ANK 1.	CC DR HSPD; Q00420; 1AMC.
FT	REPEAT 37 65 ANK 2.	CC DR MIM; 106410; -.
FT	REPEAT 69 98 ANK 3.	CC DR InterPro; IPP002110; ANK_Pfan; PF00023; ank; 4.
FT	REPEAT 102 132 ANK 4.	
FT	VARIANT 72 72 A -> P (IN BREAST CANCER; LOSS OF CDK6 INTERACTION).	
FT	SEQUENCE 168 AA; 18127 MW; 5D66AFAT15186EA CRC64;	
DB	Query Match Score 30.1%; Best Local Similarity 40.3%; Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;	CC DR CAB42644.1; -.
Qy	2 EPSADWLATAAANGRVEEVRALEAVALPNAPNSGRRPIQMMGMSARVAYELLJLHGAE	CC DR CAB42644.1; -.
Db	3 EPWNELASAAARGDLEQTLQQNYYNAQNGFERTALCYMKLGNPETARRJLRGAN	CC DR CAB42644.1; -.
Qy	62 PNCADPATLTPYDAAREGFLDTLVYLHRGARLDVDAWRGPYDABELGHRDVARY 121	CC DR CAB42644.1; -.
Db	63 PDLKD-RIGFAVHDAAARGFLDTLQTLILEQADVNIEDNGNLPIHLAAKEGLHRVVF 121	CC DR CAB42644.1; -.
Qy	122 LRAAGGTRGSNHARIDA 140	CC DR CAB42644.1; -.
Db	122 LVKHTASNVGHRNHKGDTA 140	CC DR CAB42644.1; -.
RESULT	11	DR CAB42644.1; -.
ANK2_HUMAN	ID ANK2_HUMAN; STANDARD; Q01484;	DR CAB42644.1; -.
AC	PRT; 3924 AA.	DR CAB42644.1; -.

DR	InterPro; IPR000488; Death.	Db	528 TNGYT-PULHISAREGQDVASVLLERGAHSLATKKGGFTPLHVAKYGSLLDVAKLILRR 586
DR	InterPro; IPR000905; 205.	QY	125 AAGGTGSSN 133
DR	Pfam; PF00023; ank; 24.	Db	587 : 595
DR	Pfam; PF00531; deach; 1.		
DR	Pfam; PF00791; 205; 1.		
DR	SMART; SN00242; ANK; 21.		
DR	SMART; SN00005; DEATH; 1.		
DR	SMART; SM00216; 205; 1.		
DR	PROSITE; PS50088; ANK_REPEAT; 20.		
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
KW	Cytoskeleton; Alternative splicing; Repeat; ANK repeat.		
KW	Phosphorylation; Multigene family.		
FT	REPEAT 63	RESULT 12 ANK1_MOUSE ID ANK1_MOUSE AC Q02357 DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 20-AUG-2001 (Rel. 40, Last annotation update)	
FT	REPEAT 96	ANK 1 ANK 2 ANK 3 ANK 4 ANK 5 ANK 6 ANK 7 ANK 8 ANK 9 ANK 10. ANK 11. ANK 12. ANK 13. ANK 14. ANK 15. ANK 16. ANK 17. ANK 18. ANK 19. ANK 20. ANK 21. ANK 22. ANK 23. REPEAT -RICH REGION.	
FT	REPEAT 129	DEATH DOMAIN	
FT	REPEAT 158	ANXRYIN 1 (ERYTHROCYTE ANKYRIN).	
FT	REPEAT 191	MUS MUSCULUS (Mouse).	
FT	REPEAT 220	OC	
FT	REPEAT 232	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.	
FT	REPEAT 261	NCBI_TAXID=10090;	
FT	REPEAT 265	RN [1]	
FT	REPEAT 294	RP SEQUENCE FROM N.A.	
FT	REPEAT 327	RC TISSUE=ERYTHROCYTE;	
FT	REPEAT 360	RX MEDLINE=92345717; PubMed=1386265;	
FT	REPEAT 361	RA White R.A.; Birkenmeier C.S.; Peters L.L.; Barker J.E.; Lux S.E.;	
FT	REPEAT 364	RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the regulatory domain."	
FT	REPEAT 393	RT Murine erythrocyte ankyrin cDNA: highly conserved regions of the regulatory domain."	
FT	REPEAT 426	RL Mamm. Genome 3:281-285(1992).	
FT	REPEAT 430	CC ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.	
FT	REPEAT 459	CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;	
FT	REPEAT 463	CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.	
FT	REPEAT 492	CC SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.	
FT	REPEAT 525	CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).	
FT	REPEAT 529	CC -1- PTM: ACYLATION BY PALMITIC ACID GROUP(S) (BY SIMILARITY).	
FT	REPEAT 558	CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.	
FT	REPEAT 591	CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN	
FT	REPEAT 592	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
FT	REPEAT 624	CC	
FT	REPEAT 628	CC	
FT	REPEAT 657	CC	
FT	REPEAT 660	CC	
FT	REPEAT 690	CC	
FT	REPEAT 694	CC	
FT	REPEAT 723	CC	
FT	REPEAT 727	CC	
FT	REPEAT 756	CC	
FT	REPEAT 760	CC	
FT	REPEAT 789	CC	
FT	REPEAT 782	CC	
FT	REPEAT 793	CC	
FT	DOMAIN 1773	CC	
FT	REPEAT 1950	CC	
FT	REPEAT 1773	CC	
FT	REPEAT 1784	CC	
FT	REPEAT 1796	CC	
FT	REPEAT 1797	CC	
FT	REPEAT 1808	CC	
FT	REPEAT 1809	CC	
FT	REPEAT 1820	CC	
FT	REPEAT 1821	CC	
FT	REPEAT 1832	CC	
FT	REPEAT 1833	CC	
FT	REPEAT 1844	CC	
FT	REPEAT 1845	CC	
FT	REPEAT 1856	CC	
FT	REPEAT 1857	CC	
FT	REPEAT 1867	CC	
FT	REPEAT 1868	CC	
FT	REPEAT 1879	CC	
FT	REPEAT 1880	CC	
FT	REPEAT 1891	CC	
FT	REPEAT 1892	CC	
FT	REPEAT 1902	CC	
FT	REPEAT 1914	CC	
FT	REPEAT 1915	CC	
FT	REPEAT 1926	CC	
FT	REPEAT 1938	CC	
FT	REPEAT 1927	CC	
FT	REPEAT 1939	CC	
FT	REPEAT 1950	CC	
FT	DEATH DOMAIN 3536	DEATH.	
FT	3620	Q->QFLGKLHLPTAPPNEGEISLVSRLQLGPCTK	
FT	1039	(IN ISOFORM 2 AND ISOFORM 3).	
FT	1039	MISSING (IN ISOFORM 2 AND ISOFORM 3).	
FT	1444	GQ->PE (IN REF. 4).	
FT	1444	I->S (IN REF. 2).	
FT	475	I->S (IN REF. 2).	
FT	476	QY->HA (IN REF. 2).	
FT	CONFLICT 971	I->Y (IN REF. 2).	
FT	971	3582	
FT	3582	I->Y (IN REF. 2).	
FT	3586	3586	
SQ	SEQUENCE 3924 AA;	52AC496CA28E29d2 CRC64;	
SQ	430337 MW;	52AC496CA28E29d2 CRC64;	
Query Match	20.8%	Score 158; DB 1; Length 3924;	
Best Local Similarity	37.2%	Pred. No. 5.9e-07;	
Matches 4B:	Conservative 18;	Mismatches 59; Indels 4; Gaps 3;	
QY	8 LATAAARGVEEVRALEAVALPNAPNSYGRRPQLV-MMMGMSARVAELLHGAEPNCAO	66	
Db	468 LHMAAAGQVEVCLRLRDAAREQTPHIAASLGKEIVQLQIMAHPPAT	527	
QY	67 PATLTPRVHDAAREGFLDPLVVLHRAGAQLDVRDAWRGLPVDAELGHDRVARYL-RA	124	

RA	Cheung M.C., Kan Y.W., Palek J.;
RT	"cDNA sequence for human erythrocyte ankyrin.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734 (1990).
[3]	
RN	VARIANT HS ILE-462;
RP	MDME=06225A50; PubMed=8640229;
RX	Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
RA	Dorrell M., Herbers J., Kugler W., Ozcan R., Pekranc A.,
RA	Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT	"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
RT	Nat. Genet. 13:214-218 (1996).
CC	-1 - FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE NA-K ATPASE; TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC	ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTE ANION EXCHANGE PROTEIN;
CC	THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC	-1 - SUBCELLULAR LOCATION: CITOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.
CC	-1 - ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY ALTERNATIVE SPlicing. THE SEQUENCE SHOWN IS THAT OF ANKYRIN VARIANT 2.1.
CC	-1 - PTM: REGULATED BY PHOSPHORYLATION.
CC	-1 - PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC	-1 - DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).
CC	-1 - SIMILARITY: CONTAINS 23 ANK REPEATS.
CC	-1 - SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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DR	EMBL; X16609; CAA34610; 1; .
DR	EMBL; M38880; AAA51732; 1; .
DR	S03275; SJHUK.
DR	PIR; A35449; A35049.
DR	HSSP; Q00420; 1ANW.
DR	MIM; 183900; .
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR000906; 2U5.
DR	Pfam; PF00023; ank; 23.
DR	Pfam; PF00531; death; 1.
DR	Pfam; PF00791; 2U5; 1.
DR	SMART; SM00248; ANK; 22.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00218; 2U5; 1.
DR	PROSITE; PS50088; ANK_REPEAT; 20; .
DR	PROSITE; PS50297; ANK REP_REGION; .
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
KW	Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW	Phosphorylation; Lipoprotein; Multigene family; Disease mutation; Elliptocytosis; Polymorphism.
FT	INT_MET DOMAIN 0 0 89 KDA DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
FT	DOMAIN 1 826 62 KDA DOMAIN (SPECTRIN BINDING DOMAIN).
FT	DOMAIN 827 1381 55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
FT	DOMAIN 1382 1880
FT	REPEAT 43 72
FT	REPEAT 76 105
FT	REPEAT 109 138
FT	REPEAT 142 171
FT	REPEAT 173 200
FT	REPEAT 173 200

Query Match										
Best Local Similarity		Score		DB		Length				
Matches		35.4%		133.5;		1880;				
52; Conservative		15;		MisMatches		69;		Indels		
Gaps										
QY	8	LATAAAGRVEEVRAILLEAVALPNAPNNSYGRPIQV-MMMGSARYAELLLLLHGABPNCA	D	506	LTAARECHVENVLAILLEKEASQACTMKKGFTPLHAGARLDVDRWDW-GRLPVLDLAEELGHDVARYL-	-	17.6%	Score	133.5;	
Db	67	PATLTPRYPHDAAREGFLDTL-VVLHAGARLDVDRWDW-GRLPVLDLAEELGHDVARYL-	QY	67	PATLTPRYPHDAAREGFLDTL-VVLHAGARLDVDRWDW-GRLPVLDLAEELGHDVARYL-	-	34	Created	1996	
Db	566	KNGLT-PLHVAYVHNNDIVKULLPRGGG--PHSPAWNNGTPLHIAKQNEVARSILQLQ	Db	623	YGGSANAAESVQGVTPHLAAQEGHAA	146	1.22	Last sequence update	01-OCT-1997	(Rel. 34)
QY	123	--RAAAGGTROSNSNHARIDAAGPSDI	Db	623	YGGSANAAESVQGVTPHLAAQEGHAA	649	622	Last annotation update	01-NOV-1997	(Rel. 35)
RESULT	15	DAPK_HUMAN	ID	DAPK_HUMAN	STANDARD;	PRT;	1431 AA.			
AC	P53355;									
DT	01-OCT-1996	(Rel.	34							
DT	01-AUG-2001	(Rel.	40,							
DE	DEATH-ASSOCIATED PROTEIN KINASE 1	(EC	2.7.1.-						(DAP KINASE 1).	
GN	DAPK	ORF	of	DAPK						

Query Match

GN Cdkn2a OR E1ALPHA OR P16INK4A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2N; TISSUE=SPLLEEN;
 RX MEDLINE=98151529; PubMed=9482902;
 RA "Zhang S., Ramsay E.S., Mock B.A.;
 RT "Cdkn2a, the cyclin dependent kinase inhibitor encoding p16INK4a and
 p19Arf, is a candidate for the plasmacytoma susceptibility locus,
 Rptrl.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [2]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RX MEDLINE=91179476; PubMed=9021155;
 RA Herzog C.R., You M.;
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
 suppressor gene.";
 RL Mamm. Genome 8:65-66(1997).
 RN [3]
 RP SEQUENCE OF 1-155 FROM N.A.
 RC STRAIN=C57BL/6J X DBA;
 RA Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
 RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
 RL Submitted (JAN-1997) to the EMBL/CenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=DBA/2 AND C57BL/6;
 RX MEDLINE=95380169; PubMed=7651726;
 RA Quelle D.E., Ashmun R.A., Beach D., Hannon G.J., Rehberger P.A., Trono D.,
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
 RA "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
 RL Oncogene 11:655-645(1992).
 RN [5]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=DBA/2, AND C57BL/6;
 RA Gressani K.M., Rollins L.A., Miller M.S.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE OF 1-11 FROM N.A.
 RC STRAIN=ICR SWISS;
 RX MEDLINE=97128829; PubMed=8973369;
 RA Soloff E.V., Herzog C.R., You M.;
 RT "The 5'-flanking region of the El alpha form of the murine p16INK4a
 (Mr51) gene." / Gene 180:213-215(1996).
 RN [7]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=CAST/Ei, C57BL/6J, ARF/J, AND MOLF/BI;
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
 RA Pellicer A., Fernandez-Piqueras J.;
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
 in mouse inbred strains";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
 DR AF04336; AAC08961; -.
 DR EMBL; U42280; AAC00052; -.
 DR EMBL; U66087; AAB39600; JOINED.
 DR EMBL; AF004588; AAB39600; -.
 DR EMBL; U47018; AAC52987; -.
 DR EMBL; U79628; AAD00226; -.
 DR EMBL; U79628; AAD00223; -.
 DR EMBL; U79627; AAD00225; -.
 DR HSSP; P42771; -.
 DR MGDB; MGI:104738; Cdkn2a.
 DR InterPro; IPRO02110; ANK.
 DR SMART; SN00248; ANK; 1.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW Kinase; Cyclin.

GN Cdkn2a OR E1ALPHA OR P16INK4A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2N; TISSUE=SPLLEEN;
 RX MEDLINE=98151529; PubMed=9482902;
 RA "Zhang S., Ramsay E.S., Mock B.A.;
 RT "Cdkn2a, the cyclin dependent kinase inhibitor encoding p16INK4a and
 p19Arf, is a candidate for the plasmacytoma susceptibility locus,
 Rptrl.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [2]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=C57BL/6J X DBA;
 RX MEDLINE=98151529; PubMed=9482902;
 RA Zhang S., Ramsay E.S., Mock B.A.;
 RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
 p19Arf, is a candidate for the plasmacytoma susceptibility locus,
 Rptrl.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [3]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=BALB/CANPT; TISSUE=SPLEEN;
 RX MEDLINE=98151529; PubMed=9482902;
 RA Zhang S., Ramsay E.S., Mock B.A.;
 RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
 p19Arf, is a candidate for the plasmacytoma susceptibility locus,
 Rptrl.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CANPT; TISSUE=SPLEEN;
 RX MEDLINE=98151529; PubMed=9482902;
 RA Zhang S., Ramsay E.S., Mock B.A.;
 RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
 p19Arf, is a candidate for the plasmacytoma susceptibility locus,
 Rptrl.";
 RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [5]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=MA/M4J;
 RX MEDLINE=97179476; PubMed=9021155;
 RA Herzog C.R., You M.;
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
 suppressor gene." / Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [6]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=MA/M4J;
 RX MEDLINE=97179476; PubMed=9021155;
 RA Herzog C.R., You M.;
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
 suppressor gene." / Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [7]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=MA/M4J;
 RX MEDLINE=97179476; PubMed=9021155;
 RA Herzog C.R., You M.;
 RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
 suppressor gene." / Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434 (1998).
 RN [8]
 RP SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=BALB/CJ AND MUS MUS POSCHIAVINUS;
 RX MEDLINE=98151529; PubMed=9482902;
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
 RA Pellicer A., Fernandez-Piqueras J.;
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
 in mouse inbred strains.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR AF04335; AAC08962; -.
 DR EMBL; U49229; AAC00051; -.
 DR EMBL; U79628; ADD00244; -.
 DR HSSP; P55273; IBD8.
 DR MGDB; MGI:104738; Cdkn2a.
 DR InterPro; IPRO02110; ANK.
 DR SMART; SM00248; ANK; 1.
 DR PROSITE; PS50297; ANK REP REGION; 1.
 KW Kinase; Cyclin.

Query Match 62.4%; Score 474; DB 11; Length 168;

Best Local Similarity 63.2%; Pred. No. 8.2e-34;	Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;	SEQUENCE FROM N.A. STRAIN=LARGE WHITE; RA Le Chalony C.; Hayes H.; Frelat G.; Geffrotin C.; RT "Identification and mapping of swine CDKN2A and CDKN2B exon 2 sequences." RT Submitted (JUN-1989) to the EMBL/GenBank/DBJ databases.
Qy 1 NEPSADKLTAAARGVEEVALLEAVALNPNSYGRPIQVMGMSARVAELLIGCA 60	DR IUPAC: A1242737; CAB65454.1; -	
Db 1 MESAADRLARAAGAQVPDVALLERGVSPVAPNSFGRPIQVMGMSARVAELLNGCA 60	DR HSSP: P42771; 1BIT1.	
Qy 61 GRPCADPATLRRPVHDAARECFDLTLLVLRAGARDVLDLAEELGHRYDAR 120	DR InterPro: IPR002110; ANK.	
Db 61 DSNCEDDTFFSRPVHDAARECFDLTLLVLRAGARDVLDLAEELGHRYDAR 120	DR Pfam: PF00023; ank; 2.	
Qy 121 YLRAA-----AGGT - RGSNHARIDAEGSDIP 147	DR PROSITE; PS50297; ANK REP_REGION; 1.	
Db 121 YLRSAGCSLCSAGWSLCTAGNAQTDGHFSSSSTP 155	KW Kinase; cyclin.	
RESULT 7	FT NON_TER 103 103 AA; 11023 MW; 5D23ABC1088DE0B CRC64;	KW sequence 103 AA; 11023 MW;
Q9XS51 ID Q9XS51; PRELIMINARY; PRT; 102 AA.	Query Match 58.4%; Score 444; DB 6; Length 103;	SEQUENCE FROM N.A.
AC 09XS51; 01-NOV-1999 (TRIMBLrel. 12, Created)	Best Local Similarity 84.3%; Pred. No. 1.8e-31;	RP TISSUE=PBMC;
DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)	Matches 86; Conservative 5; Mismatches 11; Indels 0; Gaps 0;	RA
DE P16/CDKN2A/MTS1 (FRAGMENT).	Qy 43 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 102	RT Q9XS52; PRELIMINARY;
OS Felis silvestris catus (Cat).	Db 1 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 60	RT 01-NOV-1999 (TRIMBLrel. 12, Created)
OC Mammalia; Butheria; Carnivora; Fissipedia; Felidae; Felis.	Qy 103 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEGPS 144	RT 01-NOV-1999 (TRIMBLrel. 12, Last sequence update)
RN [1]	Db 61 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEGPS 144	DE P15/MTS2/CDKN2B (FRAGMENT).
RP SEQUENCE FROM N.A.	OS Felis silvestris catus (Cat).	OS Felis silvestris catus (Cat).
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watarai T., Tsujimoto H., Hasegawa A.;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.	OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RA "Cloning and chromosomal mapping of the feline genes p16 (MTS1/CDKN2A) and p15 (MTS2/CDKN2B)." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	DR InterPro: IPR002110; ANK.	NCBI_TAXID=9885;
RT and p15(MTS2/CDKN2B)." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	DR Pfam: PF00023; ank; 3.	RN [1]
RL AB010807; BAA35340.1; -	DR PROSITE; PS50297; ANK REP_REGION; 1.	RP SEQUENCE FROM N.A.
DE HSSP; P42771; 1BIT1.	FT NON_TER 102 102 AA; 10824 MW; 26399FF21359F35D CRC64;	RC TISSUE=PBMC;
DR InterPro: IPR002110; ANK.	DR Nishigaki K., Watarai T., Tsujimoto H., Hasegawa A.;	RA
DR Pfam: PF00023; ank; 3.	DR "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A) and p15(MTS2/CDKN2B)." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	RT
FT NON_TER 102 102 AA; 10824 MW; 26399FF21359F35D CRC64;	DR InterPro: IPR002110; ANK.	RT and P15(MTS2/CDKN2B)." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
SEQUENCE: Q9XS51	Qy 43 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 102	DR InterPro: IPR002110; ANK.
RESULT 8	Db 1 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 60	DR Pfam: PF00023; ank; 2.
Q9TSY1 ID Q9TSY1; PRELIMINARY; PRT; 103 AA.	Qy 103 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEG 142	DR PROSITE; PS50297; ANK REP_REGION; 1.
AC Q9TSY1; 01-MAY-2000 (TRIMBLrel. 13, Created)	Db 61 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEG 100	FT NON_TER 1 1 86 AA; 9340 MW; A59FE0193290E867 CRC64;
DT 01-MAY-2000 (TRIMBLrel. 13, Last sequence update)	Qy 43 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 102	SQ Sequence 86 AA; 9340 MW;
DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).	Db 1 VMMGGSARVAELLHGAEPCNADPATLRRPVHDAARECFDLTLLVLRAGARDVDAW 60	Query Match 56.2%; Score 427; DB 6; Length 86;
GN CDPN2A.	Qy 103 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEG 127	Best Local Similarity 97.6%; Pred. No. 4.4e-30;
OS Sus scrofa (Pig)	Db 61 GRLPVDLAELGLHRDVARYLRAAGGTRGSNHARIDAEG 85	Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OC Mammalia; Butheria; Carnivora; Cetartiodactyla; Suina; Suidae; Sus.	RESULT 10	Q9TSY1 ID Q9TSY1; PRELIMINARY; PRT; 103 AA.
NCBI_TAXID=9823;	Q9TSY1 ID Q9TSY1; PRELIMINARY; PRT; 103 AA.	AC 09TSY1; 01-MAY-2000 (TRIMBLrel. 13, Created)
OX	AC 09TSY1; 01-MAY-2000 (TRIMBLrel. 13, Last sequence update)	DT 01-MAY-2000 (TRIMBLrel. 13, Last annotation update)
OX NCBI_TAXID=9823;	AC 09TSY1; 01-MAY-2000 (TRIMBLrel. 17, Last annotation update)	DT 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
OX NCBI_TAXID=9823;	AC 09TSY1; 01-MAY-2000 (TRIMBLrel. 17, Last annotation update)	DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).

RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
DR EMBL; AJ242788; CAB65455.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9236 MW; 16EF7A223293CCF9 CRC64;
Query Match 53.6%; Score 407; DB 6; Length 86;
Best Local Similarity 92.9%; Pred. No. 2.4e-28;
Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 43 VMMGGSARVAELLLHGAEPICADPATLTRYVHDAREGFLDTLVLRAGARLDVRDAW 102
Db 1 VMMGGSARVAELLLHGAEPICADPATLTRYVHDAREGFLDTLVLRAGARLDVRDAW 60
Qy 103 GRLPVDLAEEGLHRDVARYLRAAG 127
Db 61 GRLPVDLAEEGLHRDVARYLRAAG 85
RESULT 14
ID 054846 PRELIMINARY; PRT; 86 AA.
AC DT 01-JUN-1998 (TRIMBLrel. 06, Created)
AC DT 01-JUN-1998 (TRIMBLrel. 06, Last sequence update)
AC DT 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N A.
RC STRAIN=C57BL/6J.
RA Malumbres M.; Pellicer A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF015460; AAB94534.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50297; ANK REP REGION; 1.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
Query Match 53.3%; Score 405; DB 11; Length 86;
Best Local Similarity 91.9%; Pred. No. 3.6e-28;
Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 43 VMMGGSARVAELLLHGAEPNCADPATLTRYVHDAREGFLDTLVLRAGARLDVRDAW 102
Db 1 VTMMSAQAVELLLHGAEPNCADPATLTRYVHDAREGFLDTLVLRAGARLDVRDAW 60
Qy 103 GRLPVDLAEEGLHRDVARYLRAAG 127
Db 61 GRLPVDLAEEGLHRDVARYLRAAG 85
RESULT 15
ID Q9Z1C2 PRELIMINARY; PRT; 113 AA.
AC Q9Z1C2;
DR 01-MAY-1999 (TRIMBLrel. 10, Created)
DR 01-JUN-2001 (TRIMBLrel. 10, Last sequence update)
DR 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P16.
OS Mus spretus (western wild mouse).

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OM protein - protein search, using sw model

Run on : May 7, 2002, 12:23:49 ; Search time 23.63 Seconds
(without alignments)

463,938 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760

Sequence: 1 MEPSADWLTAAAGRVEEV.....TRGSNHARIDAEGPSDIDP 148

Scoring table: BL0SUM62

Gapext 0.5

Searched: 522463 seqs; 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /SDS8/seqdata/geneseq/geneseq/AA1984.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	760	100.0	148	16 AAR81701	Multiple tumour su
2	760	100.0	148	16 AAR81940	Human multiple tum
3	760	100.0	151	15 AAR51401	Inhibitor of cycli
4	760	100.0	156	16 AAR85116	Cell-cycle regulat
5	760	100.0	156	20 AAY24741	Human INK-4 protei
6	760	100.0	156	21 AAY83354	Human cell cycle r
7	760	100.0	391	18 AAW25534	CDK inhibitory fus
8	760	100.0	391	20 AAW9094	Human p27/p16 fusi
9	760	100.0	391	21 AAY9526	Human W3 protein s
10	760	100.0	391	21 AAY9041	Antiproliferative
11	760	100.0	391	21 AAY96068	Angiogenesis inhib

Tumour suppressor	12	753	99.1	156	18 AAM10627
Human multiple tum	13	753	99.1	156	19 AAW19251
Amino acid sequenc	14	753	99.1	156	19 AAW74549
Human MTS1 protein	15	753	99.1	156	19 AAW40524
A human multiple t	16	753	99.1	156	20 AAW80524
Human MTS1 protein	17	753	99.1	156	21 AAF15498
Human p16 protein	18	753	99.1	156	21 AAW97524
Human cyclin depen	19	753	99.1	156	21 AAM96053
Human cyclin depen	20	753	99.1	156	21 AAY96067
Human multiple tum	21	753	99.1	156	21 Human multiple tum
Human MTS1 protein	22	753	99.1	156	21 Human MTS1 protein
Human multiple tum	23	753	99.1	156	21 Human multiple tum
Human W9 protein s	24	753	99.1	156	21 Human W9 protein s
Antiproliferative	25	753	99.1	156	21 Angiogenesis inhibit
Angiogenesis inhibit	26	753	99.1	156	22 Human W10 protein
Truncated p27/p16	27	753	99.1	156	22 Protein encoded by
Human W9 protein s	28	753	99.1	156	22 Human W9 protein s
Antiproliferative	29	753	99.1	156	22 Angiogenesis inhibit
Angiogenesis inhibit	30	753	99.1	156	22 Human W10 protein
Human W10 protein	31	753	99.1	156	22 Human W10 protein
Antiproliferative	32	753	99.1	156	22 Truncated p27/p16
Angiogenesis inhibit	33	753	99.1	156	22 Secretable angioge
Secretable angioge	34	753	99.1	156	22 Truncated p27/p16
Truncated p27/p16	35	753	99.1	156	22 Human W8 protein
Human W8 protein s	36	753	99.1	156	22 Antiproliferative
Antiproliferative	37	753	99.1	156	22 Angiogenesis inhibit
Angiogenesis inhibit	38	753	99.1	156	22 CDK inhibitory fus
CDK inhibitory fus	39	753	99.1	156	22 Angiogenesis inhibit
Angiogenesis inhibit	40	753	99.1	156	22 Secretable angioge
Secretable angioge	41	753	99.1	156	22 Truncated p27/p16
Truncated p27/p16	42	753	99.1	156	22 Human W8 protein
Human W8 protein s	43	753	99.1	156	22 Antiproliferative
Antiproliferative	44	753	99.1	156	22 Angiogenesis inhibit
Angiogenesis inhibit	45	753	99.1	156	22 Human W10 protein
Human W10 protein	46	753	99.1	156	22 Human W10 protein
Human W10 protein	47	753	99.1	156	22 Human W10 protein
Human W10 protein	48	753	99.1	156	22 Human W10 protein
Human W10 protein	49	753	99.1	156	22 Human W10 protein
Human W10 protein	50	753	99.1	156	22 Human W10 protein
Human W10 protein	51	753	99.1	156	22 Human W10 protein
Human W10 protein	52	753	99.1	156	22 Human W10 protein
Human W10 protein	53	753	99.1	156	22 Human W10 protein
Human W10 protein	54	753	99.1	156	22 Human W10 protein
Human W10 protein	55	753	99.1	156	22 Human W10 protein
Human W10 protein	56	753	99.1	156	22 Human W10 protein
Human W10 protein	57	753	99.1	156	22 Human W10 protein
Human W10 protein	58	753	99.1	156	22 Human W10 protein
Human W10 protein	59	753	99.1	156	22 Human W10 protein
Human W10 protein	60	753	99.1	156	22 Human W10 protein
Human W10 protein	61	753	99.1	156	22 Human W10 protein
Human W10 protein	62	753	99.1	156	22 Human W10 protein
Human W10 protein	63	753	99.1	156	22 Human W10 protein
Human W10 protein	64	753	99.1	156	22 Human W10 protein
Human W10 protein	65	753	99.1	156	22 Human W10 protein
Human W10 protein	66	753	99.1	156	22 Human W10 protein
Human W10 protein	67	753	99.1	156	22 Human W10 protein
Human W10 protein	68	753	99.1	156	22 Human W10 protein
Human W10 protein	69	753	99.1	156	22 Human W10 protein
Human W10 protein	70	753	99.1	156	22 Human W10 protein
Human W10 protein	71	753	99.1	156	22 Human W10 protein
Human W10 protein	72	753	99.1	156	22 Human W10 protein
Human W10 protein	73	753	99.1	156	22 Human W10 protein
Human W10 protein	74	753	99.1	156	22 Human W10 protein
Human W10 protein	75	753	99.1	156	22 Human W10 protein
Human W10 protein	76	753	99.1	156	22 Human W10 protein
Human W10 protein	77	753	99.1	156	22 Human W10 protein
Human W10 protein	78	753	99.1	156	22 Human W10 protein
Human W10 protein	79	753	99.1	156	22 Human W10 protein
Human W10 protein	80	753	99.1	156	22 Human W10 protein
Human W10 protein	81	753	99.1	156	22 Human W10 protein
Human W10 protein	82	753	99.1	156	22 Human W10 protein
Human W10 protein	83	753	99.1	156	22 Human W10 protein
Human W10 protein	84	753	99.1	156	22 Human W10 protein
Human W10 protein	85	753	99.1	156	22 Human W10 protein
Human W10 protein	86	753	99.1	156	22 Human W10 protein
Human W10 protein	87	753	99.1	156	22 Human W10 protein
Human W10 protein	88	753	99.1	156	22 Human W10 protein
Human W10 protein	89	753	99.1	156	22 Human W10 protein
Human W10 protein	90	753	99.1	156	22 Human W10 protein
Human W10 protein	91	753	99.1	156	22 Human W10 protein
Human W10 protein	92	753	99.1	156	22 Human W10 protein
Human W10 protein	93	753	99.1	156	22 Human W10 protein
Human W10 protein	94	753	99.1	156	22 Human W10 protein
Human W10 protein	95	753	99.1	156	22 Human W10 protein
Human W10 protein	96	753	99.1	156	22 Human W10 protein
Human W10 protein	97	753	99.1	156	22 Human W10 protein
Human W10 protein	98	753	99.1	156	22 Human W10 protein
Human W10 protein	99	753	99.1	156	22 Human W10 protein
Human W10 protein	100	753	99.1	156	22 Human W10 protein
Human W10 protein	101	753	99.1	156	22 Human W10 protein
Human W10 protein	102	753	99.1	156	22 Human W10 protein
Human W10 protein	103	753	99.1	156	22 Human W10 protein
Human W10 protein	104	753	99.1	156	22 Human W10 protein
Human W10 protein	105	753	99.1	156	22 Human W10 protein
Human W10 protein	106	753	99.1	156	22 Human W10 protein
Human W10 protein	107	753	99.1	156	22 Human W10 protein
Human W10 protein	108	753	99.1	156	22 Human W10 protein
Human W10 protein	109	753	99.1	156	22 Human W10 protein
Human W10 protein	110	753	99.1	156	22 Human W10 protein
Human W10 protein	111	753	99.1	156	22 Human W10 protein
Human W10 protein	112	753	99.1	156	22 Human W10 protein
Human W10 protein	113	753	99.1	156	22 Human W10 protein
Human W10 protein	114	753	99.1	156	22 Human W10 protein
Human W10 protein	115	753	99.1	156	22 Human W10 protein
Human W10 protein	116	753	99.1	156	22 Human W10 protein
Human W10 protein	117	753	99.1	156	22 Human W10 protein
Human W10 protein	118	753	99.1	156	22 Human W10 protein
Human W10 protein	119	753	99.1	156	22 Human W10 protein
Human W10 protein	120	753	99.1	156	22 Human W10 protein
Human W10 protein	121	753	99.1	156	22 Human W10 protein
Human W10 protein	122	753	99.1	156	22 Human W10 protein
Human W10 protein	123	753	99.1	156	22 Human W10 protein
Human W10 protein	124	753	99.1	156	22 Human W10 protein
Human W10 protein	125	753	99.1	156	22 Human W10 protein
Human W10 protein	126	753	99.1	156	22 Human W10 protein
Human W10 protein	127	753	99.1	156	22 Human W10 protein
Human W10 protein	128	753	99.1	156	22 Human W10 protein
Human W10 protein	129	753	99.1	156	22 Human W10 protein
Human W10 protein	130	753	99.1	156	22 Human W10 protein
Human W10 protein	131	753	99.1	156	22 Human W10 protein
Human W10 protein	132	753	99.1	156	22 Human W10 protein
Human W10 protein	133	753	99.1	156	22 Human W10 protein
Human W10 protein	134	753	99.1	156	22 Human W10 protein
Human W10 protein	135	753	99.1	156	22 Human W10 protein
Human W10 protein	136	753	99.1	156	22 Human W10 protein
Human W10 protein	137	753	99.1	156	22 Human W10 protein
Human W10 protein	138	753	99.1	156	22 Human W10 protein
Human W10 protein	139	753	99.1	156	22 Human W10 protein
Human W10 protein	140	753	99.1	156	22 Human W10 protein
Human W10 protein	141	753	99.1	156	22 Human W10 protein
Human W10 protein	142	753	99.1	156	22 Human W10 protein
Human W10 protein	143	753	99.1	156	22 Human W10 protein
Human W10 protein	144	753	99.1	156	22 Human W10 protein
Human W10 protein	145	753	99.1	156	22 Human W10 protein
Human W10 protein	146	753	99.1	156	22 Human W10 protein
Human W10 protein	147	753	99.1	156	22 Human W10 protein
Human W10 protein	148	753	99.1	156	22 Human W

DR N-PSDB; AAT00736.
 XX Detecting polymorphism associated with cancer predisposition - also
 PT DNA, vectors and host cells e.g. for gene or protein replacement
 PR therapy and drug screening
 XX Example 8; Pages 92-93; 148pp; English.

CC An individual can be diagnosed as having a predisposition to cancer
 CC by detecting an alteration in the wild type multiple tumour
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1
 CC gene ORF AAT00736 (which encodes AAT01701) mutant sequences AAT00749/50.
 CC The above assay can also be used in the diagnosis and prognosis of
 CC melanoma, lymphoma, breast and thyroid
 CC cancers, etc..
 XX Sequence 148 AA;

Query	Match	Score	Length
Best	Local Similarity	100.0%	148;
Matches	Conservative	100.0%	Score 760; DB 16;
Qy	MEPSADWLTAAARGVEEVRAVALLAVALPNAPNSYGRRPQYMMGSGARVAELLHLHGA	100.0%	Length 148;
Db	1 mepsadwltaaargveevraavallalavpnapsygrrpqymmgsgarvaelllhga	100.0%	
Qy	EPNCADPATLTRPVHDAAREGFLDTLVYLHRAGARDVDAWGRLPVDAELGLHDRV	100.0%	
Db	1 epncadpatlrvphdaaregfltdtvylhragarldvrdawgrlpvdlaelghdrv	100.0%	
Qy	YDRAAAGCTRGSNHARDAAEGPSDIPD	100.0%	
Db	1 ydraaaggtrgsnharidaaaegpsdipd	100.0%	

RESULT 2
 ID AAR80940 standard; Protein; 148 AA.

XX

AC AAR80940;

XX DT 03-MAY-1996 (first entry)

XX DE Human multiple tumour suppressor polypeptide, MTS1.

XX KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;

XX KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;

XX KW gene therapy; chronic.

OS Homo sapiens.

PN WO9525429-A1.

XX PD 28-SEP-1995.

XX PF 17-MAR-1995;

XX XX 95WO-US03316.

XX PR 01-JUN-1994;

XX PR 18-MAR-1994;

XX PR 18-MAR-1994;

XX PR 18-MAR-1994;

XX PR 14-APR-1994;

XX PR 18-MAR-1994;

XX PR 18-MAR-1994;

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Kamb A;

XX DR WP3; 1995-344401/44.

XX DR N-PSDB; AAQ99158.

XX DR N-PSDB; AAQ63491.

XX DR Detection of subunit components of cyclin complexes - used for
 PT diagnosing transformation of a cell and developing inhibitors and

PT	Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukemia
PT	XX PS Claim 5; Page 92-93; 156pp; English.
PT	XX CC Several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence is the MTS1 polypeptide MTS1 cDNA poly peptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS1 cDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS1 polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells containing an altered MTS1 gene are useful for screening for potential cancer therapeutics.
PT	XX SQ Sequence 148 AA;
PT	XX Query Match Score 760; DB 16; Length 148;
PT	XX Best Local Similarity 100.0%; Pred. No. 4.4e-83;
PT	XX Mismatches 0; Indels 0; Gaps 0;
PT	XX Matches 148; Conservative 0; Mismatches 0;
PT	XX Matches 148; Length 148; Conserv. 0; Mismatches 0; Indels 0; Gaps 0;
PT	Qy 1 MEPSADWLTAAARGVEEVRAVALLAVALPNAPNSYGRRPQYMMGSGARVAELLHLHGA 60
PT	Db 1 mepsadwltaaargveevraavallalavpnapsygrrpqymmgsgarvaelllhga 60
PT	Qy 61 EPNCADPATLTRPVHDAAREGFLDTLVYLHRAGARDVDAWGRLPVDAELGLHDRV 120
PT	Db 1 epncadpatlrvphdaaregfltdtvylhragarldvrdawgrlpvdlaelghdrv 120
PT	Qy 61 YDRAAAGCTRGSNHARDAAEGPSDIPD 148
PT	Db 1 ydraaaggtrgsnharidaaaegpsdipd 148
PT	XX RESULT 3
PT	XX AARS53401
PT	XX ID AARS53401 standard; Protein; 151 AA.
PT	XX AC AARS53401;
PT	XX XX DE Inhibitor of cyclin dependent kinase 4 (p16INK4).
PT	XX AC AARS53401;
PT	XX XX DE Inhibitor of cyclin dependent kinase 4 (p16INK4).
PT	XX AC AARS53401;
PT	XX XX CYCLIN; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia; lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex
PT	XX OS Homo sapiens.
PT	XX PN WO9409135-A.
PT	XX XX DR 28-APR-1994.
PT	XX XX PR 18-OCT-1993; 93WO-US09945.
PT	XX XX PR 16-OCT-1992; 92US-0963308.
PT	XX PR 17-DEC-1992; 92US-091997.
PT	XX PA (COLD-) COLD SPRING HARBOR LAB.
PT	XX PI Beach DH, Xiong Y;
PT	XX XX DR WPI; 1994-151320/18.
PT	XX DR N-PSDB; AAQ63491.

FTT
XX /note= "(Gly4Ser)2 linker"
XX WO9727297-A1.
PN XX
XX PD 31-JUL-1997.
XX 17-JAN-1997; 97WO-US00569.
PR XX 23-JAN-1996; 96US-0589981.
XX PA (MITO-) MITOTIX INC.
XX PT Beach D, Gyuris J, Lamphere L;
XX DR 1997-393685/36.
XX N-PSDB; AAT74051.
XX PT Chimeric inhibitor of cyclin dependent kinase - useful for gene therapy of cancer and other proliferative and differentiative diseases
XX PS Claim 40: Page 38-40; 50pp; English.
XX CC This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKs. The protein controls proliferation and/or differentiation of cells, particularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or oogenesis. The chimeric proteins can also be used *in vitro* to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK/cyclin complex than binding motifs used individually (since they may bind to CDK involved in different stages of the cell cycle).
XX Sequence 391 AA;

XX KW Cyclin-dependent kinase; CDK; cyclin complex; inhibitory; restenosis; CKK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermogenesis; tachycardia; human; p27; p16.

XX OS Homo sapiens.
XX PN WO9906540-A2.
XX PD 11-FEB-1999.
XX PF 29-JUL-1998; 98WO-US15759.
XX PR 29-JUL-1997; 97US-0902572.
XX PA (MITO-) MITOTIX INC.
XX PI Beach DH, Gyuris J, Lamphere L;
XX DR 1999-153770/13.
XX N-PSDB; AAX26220.

PT Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers, fibrosis and neurodegeneration

PA Claim 63; Page 70-72; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the cDS to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and TCP. (A) are used to treat vascular wounds that involve a break in the endothelium and excessive proliferation of smooth muscle, particularly restenosis but more generally any repair of cardiovascular damage, arteriosclerotic lesions or for endothelialisation of synthetic vascular grafts. More generally, FP are used to treat unwanted cellular proliferation in a very wide range of situations, e.g. for treating vascular diseases as above, fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration; acne; also to control hair growth (e.g. to prevent hair loss caused by chemotherapy or radiation); periodontal disease; to treat tachycardia; to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding motifs from two or more different proteins bind to CDKs so inhibit cell cycle progression, particularly smooth muscle cell proliferation. The gene constructs may also be used to produce FP in cell cultures, for production or for regulating cell differentiation *in vitro*. The present sequence represents a human p27-p16 fusion protein.

SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 18; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-82;
Matches 148; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSSDWLATAAARGERVEVALLAEAVLPNAPSYGRPIQYMMGSAARVAVLLHGA 60
Db 244 mepsdwlataaargervevallaeavlpnapsygrpiqymmmgssarveellhga 303

Qy 61 EPNCADPATLTPYHDAAREGELDTLVYLHRAGARLDYRDANGRLPYDVLAAEELGHRYDVAR 120
Db 304 epncdpatltpyhdaregeldtvylhragardlyrdangrlpydvlaaeelghryvar 363

Qy 121 YLRAAAGGTGSGNHARIDAEGPSDIPD 148
Db 364 ylraaaggtrgsnharidaegpsdipd 391

RESULT 8
AAW95094 standard; Protein; 391 AA.
XX ID AAW95094
AC AAW95094;
XX DT 25-MAY-1999 (first entry)
XX DE Human p27-p16 fusion protein.

Query Match 100.0%; Score 760; DB 20; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-82;
Matches 148; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGERVEVALLAEAVLPNAPSYGRPIQYMMGSAARVAVLLHGA 60

Db	244	mepradvlataaargveevrallaevalpapnsvgrppiqmmngsarvaeilllhga	303	Db	304	epncadpatlrvphdaaregfdltlvrlhragarldvrdawgrlpvdlaelghrdvar	363
Qy	61	EPCADPATLTRPVHDAAREGFLDTLVLRAGARLDVRDAWGRLPVDLAELGHRDVAR	120	Qy	121	YLRAAAGGTGSNHRIDAAEGPSDIPD	148
Db	304	epncadpatlrvphdaaregfdltlvrlhragarldvrdawgrlpvdlaelghrdvar	363	Db	364	ylraaaggtrgsnhridaaegpsdipd	391
Qy	121	YLRAAAGGTGSNHRIDAAEGPSDIPD	148	RESULT	10		
Db	364	ylraaaggtrgsnhridaaegpsdipd	391	AAV96041			
RESULT	9			ID	AAY96041	standard; Protein;	391 AA.
ID	AAV97526	standard; Protein;	391 AA.	XX	XX		
XX	AAV97526;			AC	AAV96041;		
AC				XX	XX		
XX	15-JAN-2001	(first entry)		DT	05-DEC-2000	(first entry)	
XX				DE			
DE	Human W3 protein sequence.			XX			
XX				Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;			
KW	Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;			KW			
KW	adenovirus E4 protein; neoplasia; W3 protein.			P16; human; smooth muscle cell; hyperproliferation; restenosis;			
XX				KW			
OS	Homo sapiens.			XX			
XX				OS			
PN	WO200052184-A1.			Hom sapiens.			
XX				XX			
PD	08-SEP-2000.			Key			
XX				FT			
PF	01-MAR-2000; 2000WO-US053350.			Peptide			
XX				FT			
PR	01-MAR-1999; 99US-0122974.			Protein			
PR	08-APR-1999; 99US-0128221.			FT			
PR	09-APR-1999; 99US-0128515.			FT			
XX				FT			
PA	(CELL-) CELL GENESYS INC.			label = p16			
PA	(MTO-) MITOTIX INC.			XX			
XX				PN			
PI	Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;			WO200052159-A1.			
XX				XX			
DR	WPI; 2000-587315/55.			Key			
N-PSDB;	AAA90923.			FT			
XX				Protein			
XX				FT			
PR	Protein and nucleic acid compositions for preventing and treating			label = 6His-tag			
PT	PT neoplasias (particularly cancer), comprises a novel chimeric cyclin			FT			
PT	PT dependent kinase inhibitor and adenovirus E4 protein			Peptide			
XX				FT			
XX				Protein			
PS	Example 1; Page 108-109; 126pp; English.			FT			
XX				label = Hinge			
CC	This sequence represents the human W3 protein.			XX			
CC	The invention relates to a protein composition comprising a novel			CC			
CC	purified chimeric cyclin dependent kinase inhibitor (CDK1) and a			CC			
CC	purified adenovirus E4 protein. The compositions comprising the protein,			CC			
CC	or the DNA encoding it are useful for treating neoplasias in animals. The			CC			
CC	compositions also find use in assays to eliminate a specific			CC			
CC	sub-population of cultured cells to determine the susceptibility of			CC			
CC	neoplastic cells to treatment with the compositions and also in assays to			CC			
CC	CC synchronise cell growth in cultured cells.			CC			
XX				CC			
Sequence	391 AA;			CC			
SQ				CC			
Query Match	100.0%	Score 760; DB 21; Length 391;		CC			
Best Local Similarity	100.0%	Pred. No. 1..6..-82;		CC			
Matches	148; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		CC			
Qy	1	MPESDAFLATAARGVEEVRLAVALPAPNSYGRPPIQMMNGSARVAELLLLHGA	60	CC			
Db	244	mepradvlataaargveevrallaevalpapnsvgrppiqmmngsarvaeilllhga	303	CC			
Qy	61	EPCADPATLTRPVHDAAREGFLDTLVLRAGARLDVRDWGRLPVDLAELGHRDVAR	120	CC			

DR WPI; 1998-494842/42.
 DR N-PSDB; AAV53B19.

XX PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 PT useful as hybridisation probes, primers and recombinant production
 PT of MTS in the diagnosis and treatment of cancers related to MTS
 PT mutation(s)

XX Disclosure; Column 63-64; 73pp; English.

XX This is the amino acid sequence of the multiple tumour suppressor 1
 CC (MTS-1) protein, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations
 CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.

XX Sequence 156 AA;

Query Match 99.1%; Score 753; DB 19; Length 156;
 Best Local Similarity 99.3%; Pred. No. 3 3e-82;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEEVRLAEAVLPNAPNSYGRPRIQVMMGSAARVAFELLHGA 60
 Db 9 mepsadwltaaargrveevrlaeavlpnapsygrpriqvmmgssarvaeilllhga 68

Qy 61 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARDVDRDAGRLPVDLAEELGHRDVAR 120
 Db 69 epncadpatlrvphdaaregfldtvlvrhagarldvrdangrlprdlaeelghrdvar 128

Qy 121 YLRAAAGGTRGSNNHARIDAAGGPSDIPD 148
 Db 129 ylraaaggtrgsnnharidaagpsdipd 156

RESULT 15
 AAW40524 ID AAW40524 standard; Protein; 156 AA.
 XX AC AAW40524;
 XX DT 15-JUL-1998 (first entry)
 XX DE Human MTS1 protein.
 XX KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
 KW familial melanoma locus; MIM; predisposition.
 XX OS Homo sapiens.
 XX PN US5739027-A.
 XX PD 14-APR-1998.
 XX PF 07-JUN-1995; 95US-0487033.
 XX PR 07-JUN-1995; 95US-0487033.
 PR 18-MAR-1994; 94US-0214582.
 PR 18-MAR-1994; 94US-0215086.
 PR 18-MAR-1994; 94US-0215087.
 PR 14-APR-1994; 94US-0223369.
 PR 01-JUN-1994; 94US-0251938.
 PR 17-MAR-1995; 95US-0503316.
 XX PA (MYRIAD) MYRIAD GENETICS INC.

XX Kamb A;
 PI XX
 DR WPI; 1998-250421/22.
 DR N-PSDB; AAV11238.
 XX PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
 PT useful for the diagnosis of cancers related to MTS1E1-beta
 PT mutation(s) and their treatment
 XX Disclosure; Column 63-64; 72pp; English.
 XX This sequence represents a human multiple tumour suppression protein,
 CC This sequence represents a human multiple tumour suppression protein,
 CC MTS1. The MTS1 gene locus is also referred to as the familial melanoma
 CC (FIM). The MTS1 gene locus is located on human chromosome 9p21. Germ line mutations
 CC in MTS1 genes can be used in the diagnosis of predisposition to cancers,
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
 CC ovary, uterus, testis, kidney, stomach and rectum.
 XX Sequence 156 AA;
 Query Match 99.1%; Score 753; DB 19;
 Best Local Similarity 99.3%; Pred. No. 3 3e-82;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEEVRLAEAVLPNAPNSYGRPRIQVMMGSAARVAFELLHGA 60
 Db 9 mepsadwltaaargrveevrlaeavlpnapsygrpriqvmmgssarvaeilllhga 68

Qy 61 EPNCADPATLTRPVHDAAREGFDTLVVLRAGARDVDRDAGRLPVDLAEELGHRDVAR 120
 Db 69 epncadpatlrvphdaaregfldtvlvrhagarldvrdangrlprdlaeelghrdvar 128

Qy 121 YLRAAAGGTRGSNNHARIDAAGGPSDIPD 148
 Db 129 ylraaaggtrgsnnharidaagpsdipd 156

Search completed: May 7, 2002, 12:33:04
 Job time: 555 sec

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:10 ; Search time 105.99 Seconds
(without alignments)
490.476 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760

Sequence: 1 MEPSADWLATAAAGRVEEV.....TRGSNHARIDAAEGPSDIPD 148

Scoring table: BioSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:
 1: /cgn2_6/ptodata/2/paa/US080_COMB.pep: *
 2: /cgn2_6/ptodata/2/paa/US079_COMB.pep: *
 3: /cgn2_6/ptodata/2/paa/US07 COMB.pep: *
 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep: *
 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep: *
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 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep: *
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 28: /cgn2_6/ptodata/2/paa/US109_MERGED_COMB.pep1: *
 29: /cgn2_6/ptodata/2/paa/US109_MERGED_COMB.pep1: *
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 32: /cgn2_6/ptodata/2/paa/PCT_MERGED_COMB.pep1: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	760	100.0	148	Sequence 2, Appli

ALIGNMENTS

RESULT PCT-US95-03316-2
PCT-US95-03316-2
GENERAL INFORMATION:

APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF CANCER DUE TO THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Venable, Baetler, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE:

CLASSIFICATION: ; APPLICATION NUMBER: PCT/US95/03537
; PRIOR APPLICATION DATA: ; FILING DATE: ;
; APPLICATION NUMBER: US 08/251,938 ;
; FILING DATE: 01-JUN-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,938
; FILING DATE: 01-JUN-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994 ;
; ATTORNEY/AGENT INFORMATION: ;
; NAME: Saxe, Stephen A. ;
; REGISTRATION NUMBER: 38,609 ;
; REFERENCE/DOCKET NUMBER: 24884-109348-PCT-2 ;
; TELECOMMUNICATION INFORMATION: ;
; TELEPHONE: 202-962-48448 ;
; TELEFAX: 202-962-8300 ;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-03316-2

Query Match 100.0%; Score 760; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MEPSADWATAAARGRVYEVRALEAVLPNAPNSYGRPIQVMMGSARVABLLHGA 60
Db 1 MEPSADWATAAARGRVYEVRALEAVLPNAPNSYGRPIQVMMGSARVABLLHGA 60

Qy 61 EPNCADPATLTRYRPHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAELGLHDVAR 120
Db 61 EPNCADPATLTRYRPHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAELGLHDVAR 120

Qy 121 YLRAAAGTTRGSNHARDAAEGPSDIPD 148
Db 121 YLRAAAGTTRGSNHARDAAEGPSDIPD 148

RESULT 2
PCT-US95-03537-2
SEQUENCE 2, Application PCT/US9503537
GENERAL INFORMATION: ;
APPLICANT: Skolnick, Mark H. ;
APPLICANT: Cannon Albright, Lisa A. ;
APPLICANT: Kamb, Alexander ;
TITLE OF INVENTION: GERMMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: METHOD FOR THERAPY OF CANCER DUE TO
TITLE OF INVENTION: THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 36
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM: ;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: ;
APPLICATION NUMBER: US/08/214,581

RESULT 3
US-09-016-869b-35-2
SEQUENCE 2, Application US/08214581
GENERAL INFORMATION: ;
APPLICANT: Kamb, Alexander ;
TITLE OF INVENTION: METHOD FOR THERAPY OF CANCER DUE TO
TITLE OF INVENTION: THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM: ;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: ;
APPLICATION NUMBER: US/08/214,581

FILING DATE: 18-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109348
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 148 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-214-581-2

Query Match 100.0%; Score 760; DB 6; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.4e-75;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60
 Db 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120
 Db 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148
 Db 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148

Query Match 100.0%; Score 760; DB 6; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.4e-75;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60
 Db 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120
 Db 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148
 Db 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148

RESULT 5
 US-08-215-086-2
 Sequence 2, Application US/08215086
 GENERAL INFORMATION:
 APPLICANT: Cannon-Albright, Lisa A.
 COMPUTER: Skolnick, Mark H.
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/215,086
 FILING DATE: 18-MAR-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109348
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 148 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-215-086-2

Query Match 100.0%; Score 760; DB 6; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.4e-75;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60
 Db 1 MEPSADWLTAAARGVVEVRALLEAVALPNAPNSYGRPIQVMMGSARVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120
 Db 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDVDAWRGPVLDIAELGHRDVAR 120

QY 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148
 Db 121 YLRAAAGGTRGSNHRIDAAGPSDIPD 148

Db 121 YLRAAGGTGSNHRIDAEGPSDIDP 148
 RESULT 6
 US-08-215-087-2
 ; Sequence 2, Application US/08215087
 ; GENERAL INFORMATION:
 ; APPLICANT: Skolnick, Mark H.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ithnen, Jeffrey L.
 ; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER
 ; TITLE OF INVENTION: AT THE MTS GENE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue, Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/215,088
 ; FILING DATE: 18-MAR-1994
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ithnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 148 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-215-088-2

Query Match 100.0%; Score 760; DB 6; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.4e-75;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-08-215-088-2
 ; Sequence 2, Application US/08215088
 ; GENERAL INFORMATION:
 ; APPLICANT: Kamb, Alexander
 ; TITLE OF INVENTION: SCOMATIC MUTATIONS IN THE MTS GENE
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue, Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/227,369
 ; FILING DATE: 14-APR-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/214,582
 ; FILING DATE: 18-MAR-1994

Db 121 YLRAAGGTGSNHRIDAEGPSDIDP 148
 RESULT 7
 US-08-215-088-2
 ; Sequence 2, Application US/08215088
 ; GENERAL INFORMATION:
 ; APPLICANT: Kamb, Alexander
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND PROGNOSIS OF CANCER DUE TO THE MTS GENE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28, 957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-227-369-2

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWATAAARGRVEVRLLEAVALPNAPNSYGRPIQYMMGSARVAELLLHGA 60
Db 1 MEPSADWATAAARGRVEVRLLEAVALPNAPNSYGRPIQYMMGSARVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDLWRGRLPVDAEELGHDRV 120
Db 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGARDLWRGRLPVDAEELGHDRV 120

QY 121 YLRAAGGTGSGNHRIDAEGPSDIDP 148
Db 121 YLRAAGGTGSGNHRIDAEGPSDIDP 148

QY 121 YLRAAGGTGSGNHRIDAEGPSDIDP 148
Db 121 YLRAAGGTGSGNHRIDAEGPSDIDP 148

RESULT 10
US-09-480-135-16
Sequence 16, Application US/09480135
GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: INK4d-P18 and InK4d-P19, Inhibitors of Cyclin Dependent Kinases GDK4 and CDK6, and Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC
STREET: 1100 New York Ave., Suite 600, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,135
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/384,106
APPLICATION NUMBER: 08/384,106
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656-0500002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-480-135-16

Query Match 100.0%; Score 760; DB 18; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWATAAARGRVEVRLLEAVALPNAPNSYGRPIQYMMGSARVAELLLHGA 60

RESULT 11
US-09-480-135-24
; Sequence 24, Application US/09480135
; GENERAL INFORMATION:
; APPLICANT: Sherr, Ph.D., Charles J.
; APPLICANT: Downing, M.D., James
; APPLICANT: Hirai, Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPERNE, KESSLER, GOLDSTEIN & FOX, PLLC
; STREET: 1100 New York Ave., Suite 600, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,135
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIORITY NUMBER: 0656-0500002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-480-135-24

Query Match 100.0%; Score 760; DB 18; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 760; DB 28; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEVRALEAVLPAPNSGRRPQYMMGSSARVAELLLHGA 60
Db 1 MEPSADWLTAAARGRVEVRALEAVLPAPNSGRRPQYMMGSSARVAELLLHGA 60

Qy 61 EPNCADPATLTPVHDAREGFLDTLYVLHLAGRLDVRDAWGRLPVDLAEGLHDRV 120
Db 61 EPNCADPATLTPVHDAREGFLDTLYVLHLAGRLDVRDAWGRLPVDLAEGLHDRV 120

Qy 121 YLRAAGGTGSNHRIDAEGPSDIPD 148
Qy 121 YLRAAGGTGSNHRIDAEGPSDIPD 148

Db 61 EPNCADPATLTRPVHDAAREGFLDTLVLRAGRLDVRDAEGLRHDVAR 120

Qy 121 YLRAAAGTGSNSHARDAAEGPSDIPD 148
 ; Sequence 2, Application US/08248812
 ; GENERAL INFORMATION:
 ; APPLICANT: Beach, David H.
 ; APPLICANT: Demetrick, Douglas J.
 ; APPLICANT: Serrano, Manuel
 ; APPLICANT: Hannan, Gregory J.
 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses Related Thereto
 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses Related Thereto
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: LAHTE & COCKFIELD
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII(text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/306,511
 ; FILING DATE: 14-SEP-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: CSI-001CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 156 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-306-511-2

Query Match 13 Score 100.0% DB 6; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1_se-75;
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15 US-08-497214A-2
 Qy 1 MEPSADWLATAAARGRVVEVRLAEAVLPNAPNSYGRPIQYMMGSAVAFLLHGA 60
 ; Sequence 2, Application US/08497214A
 ; GENERAL INFORMATION:
 ; APPLICANT: Beach, David H.
 ; APPLICANT: Demetrick, Douglas J.
 ; APPLICANT: Serrano, Manuel
 ; APPLICANT: Hannan, Gregory J.
 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses Related Thereto
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Foley, Hoag & Eliot LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA

Db 129 YLRAAAGTGSNSHARDAAEGPSDIPD 156

Qy 121 YLRAAAGTGSNSHARDAAEGPSDIPD 148
 ; Sequence 2, Application US/08306511
 ; GENERAL INFORMATION:
 ; APPLICANT: Hannan, Gregory J.
 ; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses Related Thereto
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: Foley, Hoag & Eliot LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA

Db 129 YLRAAAGTGSNSHARDAAEGPSDIPD 156

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;
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,214A
; FILING DATE: 30-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIY071.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-497-214A-2

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	Query	Match	Best Local Similarity	Score	DB	Length
Matches	Qy	1	100.0%	760	8	156
Matches	Db	9	100.0%	1.5e-75	0	0
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Matches	Db	69	100.0%	MEPSADWLTAAARGVEEVALLEAVLPNAPNSYGRP	QVMNGSARVAELLHLGA	60
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Matches	Db	129	100.0%	EPICADPATLTPVHDAREGFDLTIVLHAGARDVYD	LPVDAELGIRDVAR	120
Matches	Qy	129	100.0%	EPICADPATLTPVHDAREGFDLTIVLHAGARDVYD	LPVDAELGIRDVAR	128
Matches	Db					

YLRRAAGCTGSNHARDAEGPSDFD 148
Db YLRRAAGCTGSNHARDAEGPSDFD 156

Search completed: May 7, 2002, 12:35:37
Job time: 207 sec

GenCore version 4.5	Sequence 2, Appli
Copyright (c) 1993 - 2000 Compugen Ltd.	Sequence 451, App
	Sequence 708, App
	Sequence 429, App
	Sequence 941, App
1 protein - protein search, using sw model	Sequence 6, Appli
run on: May 7, 2002, 12:32:40 ; Search time 8.7 Seconds (without alignments) 239,553 Million cell updates/sec	Sequence 26, Appli
title: US-09-016-869B-35	Sequence 2, Appli
perfect score: 760	Sequence 247, App
Sequence: 1 MPSADWLTAAARGRVEEV.....TRGSNHRIDAEGPSDIPD 148	Sequence 427, App
scoring table: BLOSUM62	Sequence 696, App
Gapext 0..5	Sequence 778, App
searched: 64870 seqs, 14081815 residues	Sequence 514, App
	Sequence 515, App
	Sequence 507, App
	Sequence 452, App
	Sequence 123, App
	Sequence 7, Appli
	Sequence 40, Appli

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maximum DB seq length: 2000000000

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PCT/US02/07826 ; Sequence 41, Application PC/TU0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification
; and Therapy of Ovarian Cancer
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRT-030PC
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; CURRENT FILING DATE: 2002-03-12
; CURRENT EXPIRATION DATE: 2022-03-12
; Database : Pending_Patents_AA_New.*
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3: /cgn2_6/picodata/1/paa/PUS02_NEW.COMB.pep: *
4: /cgn2_6/picodata/1/paa/PUS09_NEW.COMB.pep: *
Maximum Match 100%
Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived from analysis of the total score distribution.

במחנה נסיך

Best Local Similarity 99.3%; Pred. No. 1.1e-69;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 60
 Db 9 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 120
 Db 69 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 128

Qy 121 YLRAAGGTGSGNSNHARIDAEGPSDIDP 148
 Db 129 YLRAAGGTGSGNSNHARIDAEGPSDIDP 156

RESULT 5
 Sequence 1908, Application US/10113872
 GENERAL INFORMATION:
 / APPLICANT: Watanabe, Yoshihiro
 / APPLICANT: Henderson, Robert A.
 / APPLICANT: Kalos, Michael D.
 / APPLICANT: Sleath, Paul R.
 / APPLICANT: Vedick, Thomas S.
 / APPLICANT: Carter, Darrick
 / APPLICANT: Fanger, Gary R.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 / TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 / FILE REFERENCE: 210121_47C19
 / CURRENT APPLICATION NUMBER: US/10/113,872
 / CURRENT FILING DATE: 2002-03-28
 / NUMBER OF SEQ ID NOS: 2011
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO: 1908
 / LENGTH: 156
 / TYPE: PRT
 / ORGANISM: Homo sapiens

Best Local Similarity 99.3%; Pred. No. 1.1e-69;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 60
 Db 9 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 120
 Db 69 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 128

Qy 121 YLRAAGGTGSGNSNHARIDAEGPSDIDP 148
 Db 129 YLRAAGGTGSGNSNHARIDAEGPSDIDP 156

RESULT 7
 US-09-947-206C-12
 / Sequence 12, Application US/09947206C
 / GENERAL INFORMATION:
 / APPLICANT: Beach, D.
 / APPLICANT: Demerick, D.
 / APPLICANT: Serrano, M.
 / APPLICANT: Hannon, G.
 / TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
 / FILE REFERENCE: GPC1-P14-071
 / CURRENT APPLICATION NUMBER: US/09/947,206C
 / CURRENT FILING DATE: 2001-09-04
 / PRIOR APPLICATION NUMBER: 08/248,812
 / PRIOR FILING DATE: 1994-05-25
 / PRIOR APPLICATION NUMBER: 08/227,371
 / PRIOR FILING DATE: 1994-04-14
 / PRIOR APPLICATION NUMBER: 08/154,915
 / PRIOR FILING DATE: 1993-11-08
 / PRIOR APPLICATION NUMBER: 07/991,997
 / PRIOR FILING DATE: 1992-12-17
 / PRIOR APPLICATION NUMBER: 07/963,308
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 12
 / LENGTH: 157
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Alternate general formula representing amino acid sequence of
 / NAME/KEY: MISC_FEATURE
 / LOCATION: (1)..(157)

Best Local Similarity 99.3%; Pred. No. 1.1e-69;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 60
 Db 9 MEPSADWLTAAARGRVEVRALEAVLPNAPNSYGRPIQVMMSGARVAELLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 120
 Db 69 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDLVDLAEELGRDVAR 128

Qy 121 YLRAAGGTGSGNSNHARIDAEGPSDIDP 148
 Db 129 YLRAAGGTGSGNSNHARIDAEGPSDIDP 156

RESULT 6
 US-09-947-206D-12
 / Sequence 12, Application US/09947206D
 / GENERAL INFORMATION:
 / APPLICANT: Beach, D.
 / APPLICANT: Demerick, D.
 / APPLICANT: Serrano, M.
 / APPLICANT: Hannon, G.
 / TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
 / FILE REFERENCE: GPC1-P14-071
 / CURRENT APPLICATION NUMBER: US/09/947,206D
 / CURRENT FILING DATE: 2001-09-04
 / PRIOR APPLICATION NUMBER: 08/248,812
 / PRIOR FILING DATE: 1994-05-25
 / PRIOR APPLICATION NUMBER: 08/227,371
 / PRIOR FILING DATE: 1994-04-14
 / PRIOR APPLICATION NUMBER: 08/154,915
 / PRIOR FILING DATE: 1993-11-08
 / PRIOR APPLICATION NUMBER: 07/991,997
 / PRIOR FILING DATE: 1992-12-17
 / PRIOR APPLICATION NUMBER: 07/963,308
 / NUMBER OF SEQ ID NOS: 30
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 12
 / LENGTH: 157
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Alternate general formula representing amino acid sequence of
 / NAME/KEY: MISC_FEATURE
 / LOCATION: (1)..(157)

; OTHER INFORMATION: xaa=unknown amino acid residue
US-09-947-206C-12

OTHER INFORMATION: xaa=unknown amino acid residue
US-09-947-206C-12

Query Match 82.6%; Score 627.5; DB 5; Length 157;
Best Local Similarity 83.9%; Pred. No. 5.5e-57;
Matches 125; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
APPLICANT: Serrano, M.

APPLICANT: Hannon, G.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPCI-P14-071
CURRENT APPLICATION NUMBER: US/09/947,206C
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 08/248,812
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: 08/227,371
PRIOR FILING DATE: 1994-04-14
PRIOR APPLICATION NUMBER: 08/154,915
PRIOR FILING DATE: 1993-11-08
PRIOR APPLICATION NUMBER: 07/991,997
PRIOR FILING DATE: 1992-12-17
PRIOR APPLICATION NUMBER: 07/963,308
PRIOR FILING DATE: 1992-10-16
SOFTWARE: PatentIn version 3.1
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-947-206C-4

RESULT 8
Sequence 4, Application US/09947206D

GENERAL INFORMATION:
APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
APPLICANT: Serrano, M.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPCI-P14-071
CURRENT APPLICATION NUMBER: US/09/947,206D
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 08/248,812
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: 08/227,371
PRIOR FILING DATE: 1994-04-14
PRIOR APPLICATION NUMBER: 08/154,915
PRIOR FILING DATE: 1993-11-08
PRIOR APPLICATION NUMBER: 07/991,997
PRIOR FILING DATE: 1992-12-17
PRIOR APPLICATION NUMBER: 07/963,308
PRIOR FILING DATE: 1992-10-16
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
US-09-947-206D-4

RESULT 9
Sequence 4, Application US/09947206C-4

GENERAL INFORMATION:
APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
APPLICANT: Serrano, M.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPCI-P14-071
CURRENT APPLICATION NUMBER: US/09/947,206D
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 08/248,812
PRIOR FILING DATE: 1994-05-25
PRIOR APPLICATION NUMBER: 08/227,371
PRIOR FILING DATE: 1994-04-14
PRIOR APPLICATION NUMBER: 08/154,915
PRIOR FILING DATE: 1993-11-08
PRIOR APPLICATION NUMBER: 07/991,997
PRIOR FILING DATE: 1992-12-17
PRIOR APPLICATION NUMBER: 07/963,308
PRIOR FILING DATE: 1992-10-16
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
LENGTH: 138
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: CENTRAL TROPONIN

OTHER INFORMATION: Alternate general formula representing the amino acid sequence of
; OTHER INFORMATION: CCR-protein
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(138)
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-09-947-206D-13

Query Match 50 3%; Score 382; DB 5; Length 138;
Best Local Similarity 67.2%; Pred. No. 3.5e-32;
Matches 84; Conservative 3; Mismatches 36; Indels 2; Gaps 2;

RESULT 12
US-09-947-206D-8
; Sequence 8, Application US/09947206D
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPC1-P4-071
; CURRENT APPLICATION NUMBER: US/09/947,206D
; CURRENT FILING DATE: 2001-09-04
; CURRENT APPLICATION NUMBER: 08/1991,997
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 77

Query Match 46.8%; Score 356; DB 5; Length 77;
Best Local Similarity 93.5%; Pred. No. 7.5e-30;
Matches 72; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-947-206C-13
; Sequence 13, Application US/09947206C
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Hannon, G.
; APPLICANT: Serrano, M.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; CURRENT APPLICATION NUMBER: US/09/947,206C
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 77

Query Match 46.8%; Score 356; DB 5; Length 77;
Best Local Similarity 93.5%; Pred. No. 7.5e-30;
Matches 72; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-09-947-206C-8
; Sequence 8, Application US/09947206C
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPC1-P4-071
; CURRENT APPLICATION NUMBER: US/09/947,206C
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 138

Query Match 50 3%; Score 382; DB 5; Length 138;
Best Local Similarity 67.2%; Pred. No. 3.5e-32;
Matches 84; Conservative 3; Mismatches 36; Indels 2; Gaps 2;

RESULT 12
US-09-947-206C-13
; Sequence 8, Application US/09947206C
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPC1-P4-071
; CURRENT APPLICATION NUMBER: US/09/947,206C
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; PRIOR APPLICATION NUMBER: 07/993,308
; PRIOR FILING DATE: 1992-10-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 138

Query Match 50 3%; Score 382; DB 5; Length 138;
Best Local Similarity 67.2%; Pred. No. 3.5e-32;
Matches 84; Conservative 3; Mismatches 36; Indels 2; Gaps 2;

RESULT 12
US-09-947-206D-13
; Sequence 8, Application US/09947206D
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPC1-P4-071
; CURRENT APPLICATION NUMBER: US/09/947,206D
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; PRIOR APPLICATION NUMBER: 07/993,308
; PRIOR FILING DATE: 1992-10-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 138

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; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-947-206C-8

Query Match 46.8%; Score 356; DB 5; Length 77;
Best Local Similarity 93.5%; Pred. No. 7.5e-30; Mismatches 4; Indels 0; Gaps 0;
Matches 72; Conservative 1; Software: PatentIn version 3.1

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Db 1 ALIEAGADPNALNRFGRPIQVMMAGSARVTELLLGAEPNCADPATLTPVHDAAREG 60
Qy 82 FLDTLVVLHRGARDLV 98
Db 61 FLDTLVVLHRGARDLV 77

RESULT 14
US-09-947-206D-6
; Sequence 6, Application US/09947206D
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; ATTORNEY: Demetrick, D.
; APPLICANT: Serrano, M.
; APPLICANT: Hannon, G.
; TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
; FILE REFERENCE: GPC1-PL4-0711
; CURRENT APPLICATION NUMBER: US/09/947,206D
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 08/248,812
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: 08/227,371
; PRIOR FILING DATE: 1994-04-14
; PRIOR APPLICATION NUMBER: 08/154,915
; PRIOR FILING DATE: 1993-11-08
; PRIOR APPLICATION NUMBER: 07/991,997
; PRIOR FILING DATE: 1992-12-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 6
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-947-206D-6

Query Match 43.4%; Score 330; DB 5; Length 125;
Best Local Similarity 60.7%; Pred. No. 5.8e-27; Mismatches 12; Indels 8; Gaps 2;
Matches 68; Conservative 12; Software: PatentIn version 3.1

Qy 44 MMMSGSARVAPLLLGAEPNCADPATLTPVHDAAREGFLDTLVVLHRGARDLVDAWG 103
Db 1 MMMSGNVHVAALLNYGADNSCEDPTTFSRPVHDAAREGFLDTLVVLHRGARDLVDAWG 60
Qy 104 RLPLDAAELGHARDVARYLRA-----AGGT - RGSNHARDAAEGPSDIP 147
Db 61 RLPLDAAELGHARDVARYLRSAGCSLCTAGNVAOTDGHFSSSSTP 112

Search completed: May 7, 2002, 12:35:52
Job time: 192 sec

RESULT 15
US-09-947-206C-6
; Sequence 6, Application US/09947206C
; GENERAL INFORMATION:
; APPLICANT: Beach, D.
; APPLICANT: Demetrick, D.
; APPLICANT: Serrano, M.

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Gencore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:30:35 ; Search time 12.51 Seconds
(without alignments)
266.226 Million cell updates/sec

Title: US-09-016-869B-35
Perfect score: 760
Sequence: 1 MEPSADWLATAAAGRVEEV.....TRGSNHRIDAAEGPSDIDP 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 3: /cgn2_6/ptodata/2/1aa/6A_COMBO.pep:
 4: /cgn2_6/ptodata/2/1aa/6B_COMBO.pep:
 5: /cgn2_6/ptodata/2/1aa/PCTVS-COMB.pep:
 6: /cgn2_6/ptodata/2/1aa/bactfiles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	760	100.0	148	3	US-09-384-106A-16
3	760	100.0	148	3	US-09-384-106A-24
4	760	100.0	148	5	PCT-US93-09945-4
5	760	100.0	156	2	US-09-622-610-2
6	760	100.0	156	2	US-09-306-51A-2
7	760	100.0	156	2	US-09-893-274-2
8	760	100.0	156	3	US-09-581-918A-2
9	760	100.0	156	4	US-09-346-147B-2
10	760	100.0	156	4	US-09-822-936-2
11	760	100.0	156	5	PCT-US95-04636-2
12	760	100.0	391	1	US-09-589-981-2
13	753	99.1	156	1	US-09-474-177-2
14	753	99.1	156	1	US-09-487-033-2
15	753	99.1	156	1	US-09-480-810-2
16	753	99.1	156	2	US-09-508-735-2
17	753	99.1	156	2	US-09-848-251-2
18	753	99.1	156	2	US-09-486-047-2
19	753	99.1	156	3	US-09-120-130-2
20	753	99.1	156	3	US-09-115-252-2
21	753	99.1	156	3	US-09-986-515-2
22	753	99.1	156	4	US-09-120-128-2
23	753	99.1	156	4	US-09-120-129-2
24	753	99.1	156	4	US-09-201-139-2
25	753	99.1	156	4	US-09-120-131-2
26	753	99.1	156	4	US-09-722-2
27	749.5	98.6	157	5	PCT-US96-05252-5

ALIGNMENTS

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RESULT 1
US-09-154-915-4
; Sequence 4, Application US/08154915
; Patent No. 5618669
; GENERAL INFORMATION:
;   APPLICANT: Beach, David
;   ADDRESS: LAHIVE & COCKFIELD
;   STREET: 60 State Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/154-915
;   FILING DATE: 19-NOV-1993
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/991,997
;     FILING DATE: 17-DEC-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/963,308
;       FILING DATE: 16-OCT-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/888,178
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/1993
;       FILING DATE: 26-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US 07/701,514
;       FILING DATE: 16-MAY-1993
;     REFERENCE/DOCKET NUMBER: MII-026
;     COMMUNICATION INFORMATION:
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Vincent, Matthew P.
;         REGISTRATION NUMBER: 36,709
;       TELEPHONE: (617) 227-7400
;       TELEFAX: (617) 227-5941
;     INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 148 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;
```

MOLECULE TYPE: protein
US-08-154-915-4

Query Match 100.0%; Score 760; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60
Db 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60

RESULT 3
US-08-384-106A-24
Sequence 24, Application US/08384106A;
Patent No. 6033847

GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-384-106A-16

Query Match 100.0%; Score 760; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60
Db 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60

RESULT 4
US-09-016-869b-35.rai

Qy 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARDVRLPVDLAEELGHRDVAR 120
Db 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARDVRLPVDLAEELGHRDVAR 120

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148

RESULT 3
US-08-384-106A-24
Sequence 24, Application US/08384106A;
Patent No. 6033847

GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of Cyclin Dependent Kinases CDK4 and CDK6, and uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-384-106A-24

Query Match 100.0%; Score 760; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60
Db 1 MEPSADWLTAAARGVEEVALLEAVALPNAPNSYGRPIQVMMSGARVAAELLLHGA 60

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148

PCT-US93-09945-4
; Sequence 4, Application PC/TUS93/09945
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09945
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/963, 308
; FILING DATE: 16-OCT-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/991, 997
; FILING DATE: 17-DEC-1992
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-09945-4

Query Match 100.0%; Score 760; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWATAAARGVEVRLAVALPNAPNSYGRPQYMMGSAARVAYELLHLGA 60
Db 1 MEPSADWATAAARGVEVRLAVALPNAPNSYGRPQYMMGSAARVAYELLHLGA 60

QY 61 EPNCADPATLTKEVHDAREGFLDTLVVLRAGARDVDAWRGLPVDAELGHRDVAR 120
Db 61 EPNCADPATLTKEVHDAREGFLDTLVVLRAGARDVDAWRGLPVDAELGHRDVAR 120

QY 121 YLRAAGGTGSNHRIDAEGPSDIPD 148
Db 121 YLRAAGGTGSNHRIDAEGPSDIPD 148

RESULT 5
US-08-627-610-2
; Sequence 2, Application US/08627610
; PATENT NO. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Query Match 100.0%; Score 760; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWATAAARGVEVRLAVALPNAPNSYGRPQYMMGSAARVAYELLHLGA 60
Db 9 MEPSADWATAAARGVEVRLAVALPNAPNSYGRPQYMMGSAARVAYELLHLGA 68

QY 61 EPNCADPATLTKEVHDAREGFLDTLVVLRAGARDVDAWRGLPVDAELGHRDVAR 120
Db 69 EPNCADPATLTKEVHDAREGFLDTLVVLRAGARDVDAWRGLPVDAELGHRDVAR 128

QY 121 YLRAAGGTGSNHRIDAEGPSDIPD 148
Db 129 YLRAAGGTGSNHRIDAEGPSDIPD 156

RESULT 6
US-08-306-511A-2
; Sequence 2, Application US/08306511A
; PATENT NO. 592316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Haanon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-306-511A-2

Query Match 100.0%; Score 760; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVRALEAVLPAPNSYGRP1QVMNGSARVAELLLHGA 60
Db 9 MEPSADWLTAAARGVEEVRALEAVLPAPNSYGRP1QVMNGSARVAELLLHGA 68

Qy 61 EPICADPATLTPVHDAAREGFLDTLVLRHAGARDLVRDAGRLPVDIAEGLGRDVAR 120
Db 69 EPICADPATLTPVHDAAREGFLDTLVLRHAGARDLVRDAGRLPVDIAEGLGRDVAR 128

Qy 121 YLRAAGGTRGSNHARIDAEGPSDIPD 14.8
Db 129 YLRAAGGTRGSNHARIDAEGPSDIPD 15.6

RESULT 7
US-08-893-274-2
; Sequence 2, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannan, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 10
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 17-DECEMBER 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-893-274-2

Query Match 100.0%; Score 760; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVRALEAVLPAPNSYGRP1QVMNGSARVAELLLHGA 60
Db 9 MEPSADWLTAAARGVEEVRALEAVLPAPNSYGRP1QVMNGSARVAELLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRHAGARDLVRDAGRLPVDIAEGLGRDVAR 120
Db 69 EPNCADPATLTPVHDAAREGFLDTLVLRHAGARDLVRDAGRLPVDIAEGLGRDVAR 128

Qy 121 YLRAAGGTRGSNHARIDAEGPSDIPD 14.8
Db 129 YLRAAGGTRGSNHARIDAEGPSDIPD 15.6

RESULT 8
US-08-581-918A-2
; Sequence 2, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannan, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 17-DECEMBER 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/727,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993

; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 100.0%; Score 760; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 60
Db 9 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVDAWGLPVDIAEELGHDYAR 120
Db 69 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVDAWGLPVDIAEELGHDYAR 128

Qy 121 YLRAAAGGTGSNHNHIDAAEGPSDIPD 148
Db 129 YLRAAAGGTGSNHNHIDAAEGPSDIPD 156

RESULT 12
US-08-589-981-2
; Sequence 2, Application US/08589981
; Patent No. 5,672558
; GENERAL INFORMATION:
; APPLICANT: Guris, Jeno
; APPLICANT: Lamphere, Lou
; APPLICANT: Beach, David H.
; TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,981
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-589-981-2

Query Match 100.0%; Score 760; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 5.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 60
Db 244 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 303

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVDAWGLPVDIAEELGHDYAR 120
Db 304 EPNCADPATLTPVHDAAREGFLDTLVLRAGARDVDAWGLPVDIAEELGHDYAR 363

Qy 121 YLRAAAGGTGSNHNHIDAAEGPSDIPD 148
US-08-574-177-2
; Sequence 2, Application US/08474177
; Patent No. 5624819

RESULT 13
US-08-589-981-2
; Sequence 2, Application US/08589981
; Patent No. 5,672558

Qy 1 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 60
Db 9 MEPSADWLATAAARGRVEEVALLEAVALPNAPNSYGRPQVMMMSARVAELLHGA 68

GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; STREET: Venable, Baetjer, Howard & Civiletti, LLP
; CITY: 1201 New York Avenue, Suite 1000
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/US95/03537
; APPLICATION NUMBER: 17-MAR-1995
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA: US 08/227,369
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-177-2

RESULT 14
US-08-487-033-2
Sequence 2, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-033-2

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVRLAVALPNAPNSYGRPIQMMGSAARYAELLLLHGA 60
9 MEPSADWLTAAARGVEEVRLAVALPNAPNSYGRPIQMMGSAARYAELLLLHGA 68

Qy 61 EPNCADPATLTPVDAAREGFLDTLVVLHRAGARLDVRDANGRLPVDAELGHDRV 120
Db 69 EPNCADPATLTPVDAAREGFLDTLVVLHRAGARLDVRDANGRLPVDAELGHDRV 128

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 129 YLRAAGGTRGSNHRIDAEGPSDIPD 156

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 129 YLRAAGGTRGSNHRIDAEGPSDIPD 156

Query Match 99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTAAARGVEEVRLAVALPNAPNSYGRPIQMMGSAARYAELLLLHGA 60
9 MEPSADWLTAAARGVEEVRLAVALPNAPNSYGRPIQMMGSAARYAELLLLHGA 68

Qy 61 EPNCADPATLTPVDAAREGFLDTLVVLHRAGARLDVRDANGRLPVDAELGHDRV 120
Db 69 EPNCADPATLTPVDAAREGFLDTLVVLHRAGARLDVRDANGRLPVDAELGHDRV 128

Qy 121 YLRAAGGTRGSNHRIDAEGPSDIPD 148
Db 129 YLRAAGGTRGSNHRIDAEGPSDIPD 156

RESULT 15
 US-08-80-810-2
 Sequence 2, Application US/08480810
 ; Patent No. 5801236
 ; GENERAL INFORMATION:
 ; APPLICANT: Kamb, Alexander
 ; TITLE OF INVENTION: MTSI GENE
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 ; STREET: 1201 New York Avenue, Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MED/TOM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,810
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/03316
 ; FILING DATE: 17-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/251,938
 ; FILING DATE: 01-JUN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/215,087
 ; FILING DATE: 18-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/215,086
 ; FILING DATE: 18-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/227,369
 ; FILING DATE: 14-APR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/214,582
 ; FILING DATE: 18-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 24884-109348
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 156 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-480-810-2

Db 129 |||||||YLRAAGGTRGSNHARIDAEGPSDIPD 156
 Search completed: May 7, 2002, 12:33:23
 Job time: 168 sec

Query Match 99.1%; Score 753; DB 1; Length 156;
 Best Local Similarity 99.3%; Pred. No. 1..1e-82;
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSADWLTATAAAGRVEEVRALEAVLPNAPNSYGRPIQYMMGSARVAELLLHGA 60
 Db 9 MEPSADWLTATAAAGRVEEVRALEAVLPNAPNSYGRPIQYMMGSARVAELLLHGA 68
 Qy 61 EPNCADPATLTPVHDAREGFLDTLVVLRAGARDLVRDAEGLHDYVAR 120
 Db 69 EPNCADPATLTPVHDAREGFLDTLVVLRAGARDLVRDAEGLHDYVAR 128
 Qy 121 YLRAAGGTRGSNHARIDAEGPSDIPD 148